



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 115800

TO: Diana Johannsen

Location:

Art Unit: 1634

March 3, 2004

Case Serial Number: 692077

*JCMO
JCS*

From: P. Sheppard

Location: Remsen Building

Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes

This Page Blank (uspto)

Sheppard, Paula

From: Johannsen, Diana
Sent: Wednesday, February 25, 2004 11:53 AM
To: Sheppard, Paula
Subject: RE: 09/692,077

Hi Paula:

The search results I received in this case did not include this portion of the search:

nucleotides 880-930 of SEQ ID NO: 1
nucleotides 880-930 of SEQ ID NO: 2

I really need this part of the search since the applicant's polymorphism is located in this region. Could you check to see if this portion of the search was simply not printed or not delivered?

Thanks - I appreciate your help.

Diana

-----Original Message-----

From: Sheppard, Paula
Sent: Tuesday, February 17, 2004 2:18 PM
To: Johannsen, Diana
Subject: RE: 09/692,077

Completed today.

-----Original Message-----

From: Johannsen, Diana
Sent: Tuesday, February 17, 2004 10:02 AM
To: Sheppard, Paula
Subject: FW: 09/692,077

Hello Paula -

Could you respond to this if possible? Any info would be appreciated (just trying to determine whether I can work on this one this biweek).

Thanks a lot.

-----Original Message-----

From: STIC-Biotech/ChemLib
Sent: Tuesday, February 17, 2004 10:01 AM
To: Johannsen, Diana
Subject: RE: 09/692,077

Check with Paula Sheppard.

-----Original Message-----

From: Johannsen, Diana
Sent: Tuesday, February 17, 2004 9:54 AM
To: STIC-Biotech/ChemLib
Subject: FW: 09/692,077

If possible, could you give me an estimate re: when this search might be complete?

Thank you very much, Diana

-----Original Message-----

From: Johannsen, Diana
Sent: Friday, February 06, 2004 12:04 PM
To: STIC-Biotech/ChemLib
Subject: 09/692,077

Please search the following:

01/06
2/27/04

Sheppard
3/3/04

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using SW model

Run on: March 2, 2004, 04:47:22 ; Search time 864.5 Seconds

(without alignments)
2556.963 Million cell updates/sec

Title: US-09-692-077d-1_copy_880_930

Perfect score: 1 gagagatcgaagctgaagagga.....aggaagaggaaggaagatgt 51

Sequence: 1 gagagatcgaagctgaagagga.....aggaagaggaaggaagatgt 51

Scoring table: IDENTITY NUC

Gapop 10_0, Gapext 1.0

Searched: 3470272 seqs, 2167516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank : *

1: gb_ba : *

2: gb_ncg : *

3: gb_in : *

4: gb_om : *

5: gb_ov : *

6: gb_pat : *

7: gb_ph : *

8: gb_pl : *

9: gb_pr : *

10: gb_ro : *

11: gb_atb : *

12: gb_ay : *

13: gb_un : *

14: gb_vl : *

15: em_da : *

16: em_fun : *

17: em_hum : *

18: em_in : *

19: em_mu : *

20: em_om : *

21: em_or : *

22: em_ov : *

23: em_pat : *

24: em_ph : *

25: em_pl : *

26: em_ro : *

27: em_atb : *

28: em_un : *

29: em_vl : *

30: em_hum : *

31: em_mu : *

32: em_om : *

33: em_or : *

34: em_ov : *

35: em_pat : *

36: em_ph : *

37: em_pl : *

38: em_ro : *

39: em_atb : *

40: em_un : *

41: em_vl : *

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	51	100.0	885	9	HUMA2C2	M38742 Human alpha
2	51	100.0	1030	6	HSAS35747	AJ25747 Homo sapi
3	51	100.0	1353	6	AX350489	AX350489 Sequence
4	51	100.0	2072	6	AR270618	AR270618 Sequence
5	51	100.0	2072	6	HUMADRA2BA	M34041 Human alpha
6	51	100.0	3274	6	AX548756	AX548756 Sequence
7	51	100.0	9944	9	AF005900	AF005900 Homo sapi
8	43.6	85.5	133405	10	AL662790	AL662790 Mouse DNA
9	43.6	85.5	216444	2	AC069060	AC069060 Mus muscu
10	43.4	85.1	1185	10	ASPA27259	AJ427259 Anomaluru
11	43.2	84.7	1183	4	OCAR2B	Y15946 Oryctolagus
12	43.2	84.7	1183	4	OCY16189	Y16189 Oryctolagus
13	43.2	84.7	206933	2	AC108794	AC108794 Mus muscu
14	43.2	84.7	215065	2	AC103291	AC103291 Rattus no
15	43.2	84.7	222507	2	AC112440	AC112440 Rattus no
16	43.2	84.7	226214	2	AC126653	AC126653 Rattus no
17	43.2	84.7	287497	2	AC106946	AC106946 Rattus no
18	43.2	84.7	293183	2	AC095903	AC095903 Rattus no
19	43	84.3	1191	10	CC4427260	AJ427260 Caenor ca
20	42.6	83.5	217323	2	AC115724	AC115724 Mus muscu
21	42.6	83.5	232202	2	AC115740	AC115740 Mus muscu
22	42.2	82.7	31533	10	BX465209	BX465209 Mouse DNA
23	42.2	82.7	186272	10	AL672046	AL672046 Mouse DNA
24	42.2	82.7	189624	2	AC128836	AC128836 Rattus no
25	42.2	82.7	189886	2	AC128202	AC128202 Rattus no
26	42.2	82.7	230127	10	AL691481	AL691481 Mouse DNA
27	42.2	82.7	230227	2	AC112634	AC112634 Rattus no
28	42.2	82.7	230313	2	AC120625	AC120625 Rattus no
29	42.2	82.7	268151	2	AC111391	AC111391 Rattus no
30	42	82.4	1198	4	ECAR2B	Y15945 Equus caball
31	42	82.4	185321	2	AC110324	AC110324 Rattus no
32	42	82.4	186607	2	AC140777	AC140777 Mus muscu
33	42	82.4	221135	2	AC097027	AC097027 Rattus no
34	42	82.4	225928	2	AC128094	AC128094 Rattus no
35	42	82.4	237322	2	AC123153	AC123153 Rattus no
36	42	82.4	275192	2	AC119508	AC119508 Rattus no
37	41.6	81.6	309	10	MUSTCE	M17284 Mouse trans
38	41.6	81.6	1197	4	MTE505820	AJ505820 Manis tet
39	41.6	81.6	30837	2	AC126874_4	Continuation (5 of
40	41.6	81.6	42003	2	AC145716	AC145716 Homo sapi
41	41.6	81.6	42920	2	AC145702	AC145702 Homo sapi
42	41.6	81.6	49999	6	AX015902	AX015902 Sequence
43	41.6	81.6	49999	6	AX015908	AX015908 Sequence
44	41.6	81.6	68233	6	AX695956	AX695956 Sequence
45	41.6	81.6	78449	2	AC141965	AC141965 Rattus no

ALIGNMENTS

RESULT 1

HUMA2C2

LOCUS HUMA2C2 885 bp DNA linear PRI 06-MAR-1995

DEFINITION Human alpha-2 adrenergic receptor (ADRA2C) gene, partial cde.

ACCESSION M38742

VERSION M38742.1 GI:177867

KEYWORDS alpha-2 adrenergic receptor.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 885)

AUTHORS Chang,A.C., Ho,T.F. and Chang,N.C.

TITLE In vitro amplification by polymerase chain reaction of a partial gene encoding the third subtype of alpha-2 adrenergic receptor in

Pred. No. is the number of results predicted by chance to have a

Draft entry and computer-readable sequence for [Unpublished (1990)] kindly submitted by A.C.Chang, 20-SEP-1990.

1. .885

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1.885
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/mol_type="genomic DNA"
/organism="Homo sapiens"
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1. .885

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/gene="ADRA2C"  
/codon_start=1  
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/protein_id="AAA62823.1"  
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translation="FMCESTVGTQVQLTQSLK"
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Query Match

Best Local Similarity	100.0%;	score 51;	DB 9;	length 885;
Matches	51; Conservative	0; Mismatches	0;	
		Pred. No. 0.0017;		

[illegible][illegible]

.....GGAAGAGTGT 648

Ω

LOCUS	1030 bp	DNA	linear	PRI 18-JUL-2002
DEFINITION	Homo sapiens genomic sequence surrounding NotI site, clone			
ACCESSION	HSAB325747			
	NB1-8185.			
	AI325747			

KEYWORDS
00323/4/.1 GI:15870141

Homo sapiens

REFERENCE
AUTHORS
1 (bases 1 to 100)
Kutsumoto, A. C. (1981).
Mammalia; Eutheria; Primates; Catarrhini; Homi-
nidae; Homo.
Euteleostomi; Osteichthyes; Actinopterygii; Clupeo-
morphi; Clupeidae; Clupea; Clupea pallasii.

Levitsky, V

TITLE Flanking sequences: a tool for gene discovery and verification of the human genome

AUTHORS Khaseliev, L.L., Wasserman, W., Mahlestedt, C. and Zabarovsky, E.R.

JOURNAL Nucleic Acids Res. 20 (1992) 111-117

12136098

2 (pages 1 to 1030)
Zabarovskiy, E. D.

100.0%; Score 51; DB 6; Length 2072;

Query Match	100.0%;	Score 51;	DB 9;	Length 1030,
Best Local Similarity	100.0%;	Pred. No. 0.0017;		
Matches 51; Conservative	0;	Mismatches		

[illegible][illegible]

.....:..:..:..:..:..:..:..:..:..:..:..:..:..:..:~ 149

AY35000

Sequence	1353 bp	DNA	linear	PAT 06-FEB-2002
AX350489	1 from Patent WO0179561.			

KEYWORDS: GI:18616091

Homo sapiens

REFERENCE
AUTHORS

1 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Hominidae; Homo.
Lippert C D and J A 1998

Patent: WO 0179561-A 1 25-OCT-2001.

NO 01/9361-A 1 25-OCT-2001;
Liggett, Stephen B (us)

I. 1353

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/mol_type="unassigned DNA"
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ORIGIN

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Query Match

Matched	Best Local Similarity	Score	DB 6;	Length
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0; Mismatches 0; Indels 0; Gaps 0

51

800 GAGGATGAAGCTGAAGAGGAGAAGAGGAGAGGAGAGGAAACTT

LOCUS	SEQUENCE	DEFINITION	ACCESSION
AR270618	2072 bp	DNA	linear
Sequence	1181	from patent US 6500938.	PAT 10-APR-2003
AR270618			

KEYWORDS: *ARX2/0618.1* GI:29701852

known

Unclassified.
1 (bases 1 +

composition for the

Source	Features
1	Pathway gene expression
2	Location/Qualifiers
3	Parent: US 6500938-A 1181 31-DEC-2002;

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/ mol type="genomic DNA"

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Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 51
1292 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 1342

RESULT 5
LOCUS HUMADRA2RA 2072 bp DNA linear PRI 30-OCT-1994
DEFINITION Human alpha-2-adrenergic receptor (alpha-2 c2) gene, complete cds.
ACCESSION M34041
VERSION M34041.1 GI:178197
KEYWORDS alpha-2-adrenergic receptor; plasma membrane protein;
receptor-coupled G protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 2072)
Lomasney, J.W., Lorenz, W., Allen, L.F., King, K., Regan, J.W.,
Yang-Peng, T.L., Caron, M.G. and Lefkowitz, R.J.
Expansion of the alpha-2-adrenergic receptor family: cloning and
characterization of a human alpha-2-adrenergic receptor subtype,
the gene for which is located on chromosome 2
Proc. Natl. Acad. Sci. U.S.A. 87 (13), 5094-5098 (1990)
90311349

JOURNAL
MEDLINE
PUBMED
COMMENT Original source text: Human placenta DNA, clone alpha-2 C2.
Draft entry and computer-readable sequence for [1] kindly submitted
by J.W. Lomasney, 03-MAY-1990, for release after publication.

FEATURES
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="2"
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/protein_id="AA51666.1"
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/translation="MDHDPYVQATMAAATFLILFTIRGNALVILAVTSIR
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RPOCKINDEAWYILASISGSPAPCLMLVLRVYLAKRNRGPRAGKPGGGS
KOPRDHGGKALASALPALASVARSREVENGHSKGEKEGEPEDTGRALPPMAA
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"

ORIGIN
Chromosome 2.
Query Match 100.0%; Score 51; DB 9; Length 2072;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 51
1292 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 1342

RESULT 6
AX548756 3274 bp DNA linear PAT 26-NOV-2002
LOCUS AX548756
DEFINITION Sequence 41 from Patent WO02061087.
ACCESSION AX548756

VERSION AX548756.1 GI:25813686
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
Burner, G.C., Roush, C.L. and Brown, J.P.
Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
Patent: WO 02061087-A 41 08-AUG-2002;
Lifespan BioSciences, Inc. (US)
FEATURES
source
1..3274
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN
Query Match 100.0%; Score 51; DB 6; Length 3274;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 51
880 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 930

RESULT 7
AP005900 9944 bp DNA linear PRI 05-AUG-2003
LOCUS AP005900
DEFINITION Homo sapiens alpha2B-adrenergic receptor (alpha2C2AR) gene,
complete cds.
ACCESSION AP005900
VERSION AP005900.2 GI:33439705
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 9944)
Cayla, C., Heimonen, P., Viikari, L., Schaak, S., Snajir, A.,
Bouloumie, A., Kervonen, M., Pesonen, U., Scheinin, M. and Paris, H.
Alpha2C2-adrenergic receptor gene
Unpublished
2 (bases 1 to 9944)
Cayla, C., Schaak, S., Bouloumie, A., Devedjian, J.C. and Paris, H.
Direct Submission
Submitted (29-MAY-1997) INSDERM Unit 317, Institut Louis Bugnard,
CHU Rangueil, Toulouse 31403, France
3 (bases 1 to 9944)
Cayla, C., Heimonen, P., Viikari, L., Schaak, S., Snajir, A.,
Bouloumie, A., Kervonen, M., Pesonen, U., Scheinin, M. and Paris, H.
Direct Submission
Submitted (05-AUG-2003) INSDERM Unit 317, Institut Louis Bugnard,
CHU Rangueil, Toulouse 31403, France
REMARK
COMMENT Sequence update by submitter
On Aug 5, 2003 this sequence version replaced gi:2245627.
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Location/Qualifiers
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5500..6852
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 polya_signal 8751..8756

Query Match 100.0%; Score 51; DB 9; Length 9944;
 Best Local Similarity 100.0%; Pred. No. 0.0015;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 51
 6379 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 6429

RESULT 8
 AL662790 133405 bp DNA linear ROD 26-JUL-2002
 LOCUS Mouse DNA sequence from clone RP23-53E2 on chromosome 11, complete
 DEFINITION
 ACCESSION AL662790.21 GI:22002673
 VERSION HTG.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 133405)
 Smith, M.
 Direct Submission
 Submitted (26-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquerry@sanger.ac.uk Clone request@sanger.ac.uk
 On Jul 29, 2002 this sequence version replaced gi:21955513.
 ----- Genome Center
 Center: Wellcome Trust Sanger Institute
 Web site: http://www.sanger.ac.uk
 Contact: humquerry@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >=
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em, EMBL; Sw,
 SWISSPROT; Tr, TrEMBL; Wp, WormPep; Information on the WormPep
 database can be found at
 http://www.sanger.ac.uk/Projects/C_elegans/wormpep
 from the RPI-23 Mouse PAC Library
 constructed by the group of Pieter de Jong.
 For further details see http://www.chori.org/bacpac/home.htm
 VECTOR: pBAC3.6

FEATURES
 source Location/Qualifiers
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 /clone="RP23-53E2"
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Query Match 85.5%; Score 43.6; DB 10; Length 133405;
 Best Local Similarity 92.0%; Pred. No. 0.091;
 Matches 46; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 50
 9337 GAGGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 9386

RESULT 9
 AC069060 216444 bp DNA linear HTG 18-MAR-2003
 LOCUS Mus musculus chromosome 11 clone RP23-53E2 map 11, WORKING DRAFT
 DEFINITION
 ACCESSION AC069060
 VERSION AC069060.4 GI:29029385
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Birren, B., Linton, J., Nussbaum, C., Lander, E., Abraham, H., Allen, N.,
 Boguski, M., Brown, A., Burt, A., Burt, G.,
 Campione, A., Castle, A., Choquet, Y., Colangelo, M., Collins, S.,
 Collymore, A., Cooke, P., DeArillano, K., Dewar, K., Diaz, J. S.,
 Dodge, S., Domino, M., Doyle, C., Ginde, S., Goyette, M., Graham, L.,
 Galagan, J., Gardina, S., Glendon, S., Haefford, A., Horton, L.,
 Grand-Pierre, N., Grant, G., Hago, B., Haefford, A., Horton, L.,
 Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karas, A.,
 Klein, J., Labèque, K., Lamazares, R., Landers, T., Lebecky, J.,
 Levine, R., Liu, C., Liu, G., Locke, K., MacDonald, P., Markys, N.,
 McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPherson, R.,
 Melard, J., Meneu, L., Mihova, T., Miranda, C., Mieng, V., Morrow, J.,
 Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
 O'Neill, D., Oliver, T. M., Oliver, J., Peterson, K., Pierre, N.,
 Pisanu, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
 Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
 Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talmas, J.,
 Tesfaye, S., Theodore, J., Titrill, A., Travers, X., Triggillo, J.,
 Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
 Young, G., Zainoun, J., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (17-MAY-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 216444)

TITLE
 JOURNAL
 REFERENCES
 AUTHORS
 Anderson, S., Balaban, L., Barna, N., Bastien, V., Bede, F.,
 Boguski, M., Brown, A., Burt, A., Burt, G.,
 Campione, A., Castle, A., Choquet, Y., Colangelo, M., Collins, S.,
 Collymore, A., Cooke, P., DeArillano, K., Dewar, K., Diaz, J. S.,
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 Boguski, M., Brown, A., Burt, A., Burt, G.,
 Campione, A., Cooke, P., DeArillano, K., Dewar, K., Diaz, J. S.,
 Dodge, S., Domino, M., Doyle, C., Ginde, S., Goyette, M., Graham, L.,
 Galagan, J., Gardina, S., Glendon, S., Haefford, A., Horton, L.,
 Grand-Pierre, N., Grant, G., Hago, B., Haefford, A., Horton, L.,
 Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karas, A.,
 Klein, J., Labèque, K., Lamazares, R., Landers, T., Lebecky, J.,
 Levine, R., Liu, C., Liu, G., Locke, K., MacDonald, P., Markys, N.,
 McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPherson, R.,
 Melard, J., Meneu, L., Mihova, T., Miranda, C., Mieng, V., Morrow, J.,
 Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
 O'Neill, D., Oliver, T. M., Oliver, J., Peterson, K., Pierre, N.,
 Pisanu, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
 Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
 Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talmas, J.,
 Tesfaye, S., Theodore, J.,

	indels	Gaps
1 GAGGATGAACCTGAGAGAGAAGAAAGAGAACCGCCTGGTGTTCGCCTCCGTTTG	1;	0;
		0;

RESULT 11

ACCESSION
NUMBER

REFERENCE

TITLE

CONFERENCE

JOURNAL.

REMARK
REFERENCE
AUTHORS
TITLE
JOURNAL

On Nov 17, 1999 this sequence version replaced gi:3286559.
location/Qualifiers
1. .1183

```

type="genomic DNA"
/db_xref="taxon:9986"
<1, 21183
CDS

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Local Similarity 84.7%; Score 43.2; DB 4; Length 1183;
 Conservative 93.8%; Pred. No. 0.15;

[illegible]

RESULT 12

LOCUS
DEFINITIO

DEFINITION	1183 bp	DNA	linear	MAM 02-JUL-1998
ACCESSION	Oryctolagus cuniculus gene encoding alpha adrenenergic receptor subtype 2B, partial.			
VERSION	Y16189			

SOURCE

1

NOTES

JOURNAL.

AUTHORS
TITLE

source

```

/mol_type="genomic DNA"
/db_xref="taxon:9986"
<1..21183
CDS

```

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/protein_id="CAA76115.1"
/db_xref="GI:3288562"
/db_xref="GOA:O77830"
/db_xref="newrna_db"

```

GIN
VGAHSGXMMRRRAQLSREKRFTEFLAVIVIGFVLCMPEFFFSYSLAICPQCCRVPHG
LF"

ORIGIN

[illegible]

	1	GAGGATGAAGCTGAAGAGGAGGAAACCGCCGCAATT	0 ; Gaps	0 ;
--	---	--------------------------------------	----------	-----

845 GAGGAGAAGCTGAAGAGGAGGAGGACGAGGAGGAGGAGGAGGAGCAG 48
992

100

AC108794

HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
Mus musculus (house mouse)

REFERENCE

JOURNAL

Unpublished
JOURNAL
RP23-59D8

unordered pieces.

ACCESSION
ACT103291

VERSION
ACT103291.5

KEYWORDS
HTG, HTGS_PHASE1, HTGS_DRAFT, HTGS_FULLTOP.

SOURCE
Rattus norvegicus (Norway rat)

ORGANISM
Rattus norvegicus

REFERENCE
1 (bases 1 to 215065)

AUTHORS
Allen, C., Allen, H., Metzger, M., Lee, J., Abramson, S., Adams, C., Alder, J., Alayalabech, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Blyskal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryan, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Cesaar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Dederich, D., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Gebregeorgis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Harary, Y., Havlak, P., Hawes, A., Hamill, C., Hamilton, C., Hamilton, K., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hognes, M., Hollins, B., Howell, S., Huylk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jollivet, A., Kowitz, C., Kraft, C.L., Lebow, H., Levan, J., King, L., Kovar, C., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensen, L., Louised, H., Lozano, R., Lu, X., Ma, J., Maneswari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E., McNeil, T. Z., Meenen, E., Mawhney, S., McLeod, M.P., McNeill, T. Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nait, L., Nankervis, C., Neal, D., Newton, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L., Puro, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reijth, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajls, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorrelle, R., Sosa, J., Steime, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczek, R., Wooden, H., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Weinstock, G., and Gibbs, R.A.

TITLE
Unpublished

JOURNAL
2 (bases 1 to 215065)

AUTHORS
Worley, K.C.

JOURNAL
Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE
3 (bases 1 to 215065)

AUTHORS
Rat Genome Sequencing Consortium.

JOURNAL
Submitted (09-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT

On Nov 9, 2002 this sequence version replaced g1:23268227. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both ends and sequences and whole genome table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GUSU

Center clone name: CH230-13104

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 200859 bases at least Q40

Consensus quality: 202934 bases at least Q30

Estimated insert size: 207073; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)

* NOTE: This is a 'working draft' sequence. It currently

* consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 211244: contig of 211244 bp in length

* 211245 211344: gap of unknown length

* 211345 215065: contig of 3721 bp in length.

Location/Qualifiers

1. 215065

/organism="Rattus norvegicus"

/mol_type="genomic DNA"

/db_xref="taxon:10116"

/clone="CH230-13104"

1. 1132

/note="wgs end extension"

clone end: 17"

2440 - 3721

/note="clone boundary"

clone end: 17"

site: EcorI

end sequence: BH316900"

202478 . 203219

/note="clone boundary"

clone end: Sp6

site: EcorI

end sequence: BH316902"

203592 . 205041

/note="wgs end extension"

clone end: Sp6"

209692 . 211244

/note="wgs end extension"

clone end: Sp6"

211345 . 212647

/note="wgs end extension"

clone end: Sp6"

213358 . 215065

/note="wgs end extension"

clone end: Sp6"

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

Tue Mar 2 17:00:52 2004

us-09-692-077d-1_copy_880_930.rge

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misc_feature      109071..110316
                    /note="wgs_contig"
ORIGIN
```

[illegible]

```
Search completed: March 2, 2004, 06:08:05
Job time : 866.5 secs
```


PT disease associated with the corresponding receptor comprises detecting a
 PR polymorphic site.
 XX
 PS Claim 4; Page 144; 163pp; English.
 PY

The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene (I) - (III) by detecting a polymorphic site, comprising: (a) obtaining a sample having a polynucleotide encoding an alpha-2B, alpha-2A or alpha-2C or fragment or complement of; and (b) detecting a polymorphic site comprising nucleotide positions 901-909 of (I), a site comprising cytosine or guanine at position 753 of (II) or a site comprising (9999cggggcgcg) or (b) (ggggccgcgcgcgcg) at positions 961-972 of (III). The method may be used for genotyping an alpha2B, alpha2A or alpha2C receptor gene and further used to determine whether an individual is at increased risk of developing a disease associated with alpha2B, alpha2A or alpha2C, comprising detecting a polymorphic site which correlate to disease selected from cardiovascular disease, central nervous system disease and combinations of these. In addition, the technique may be used to predict an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g. UK14304, BHT933, norepinephrine, clonidine, oxymetazoline, guanabenz, prazosin, ARC 239, rauwolfscine, idazoxan, tolazoline, phenclomine and combinations of these) or antagonist (e.g. yohimbine, the site to a predetermined response (where the response is correlated to adenylyl cyclase, MAP kinase activity, phosphorylation or inositol phosphate levels). The present sequence is that of the third intracellular loop of the human alpha-2B_{AD} (Genbank Accession AF009500), the sequence includes a 9 nucleotide polymorphic site at nucleotides 901-909, absent in the alpha-2B_{AR} variant (AA199906)

Query Match	100.0%;	Score 51;	DB 4;	Length 1353;
Best Local Similarity	100.0%;	Pred. NO. 0.00055;		
Matches 51;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Dy

1 GAGCGTGAAGCTGAAAGAGAGAAAGAGAGAGAGAGAGAGAGATGT 51
|||||
Db

880 GAGCGTGAACTGAAAGAGAGAAAGAGAGAGAGAGAGAGAGAGATGT 910

RESULT 2
AAB04762
ID
AAB04762 standard; DNA; 1353 BP.

04-JUL-2001 (first entry)

Human α 1A-adrenoceptor (α 1A-AR) gene.

MM acute myocardial infarction; AMI; Prinzmetal's variant; ds.
MM acute myocardial infarction; AMI; Prinzmetal's variant; ds.
MM coronary artery; coronary heart disease; CHD; chronic angina pectoris;
MM norepinephrine; epinephrine; therapy; vascular contraction;
MM intracellular loop; chromosome 2; catecholamine;
MM acute myocardial infarction; AMI; Prinzmetal's variant; ds.

S	Homo sapiens.
X	
H	
T	Location/Qualifiers
CDS	1..1353

```

/*tag= a
/product= "Human alpha2B-adrenoceptor (alpha2B-AR)
protein"

```

MOZ00129082-A1.
26-APR-2001.
20-OCT-2000. 200000 *****

22-OCT-1999; 99US-00422985.

PA (JUVA-) JUVANTIA PHARMA LTD OY.
XX

PI Snapir A, Heimonen P, Alhopuro P, Karvonen M, Koulu M, Pesonen U,
PI Scheinin M, Salonen JT, Tuomainen T, Lakka TA, Nyyssönen K,
PI Salonen R, Kahanen J, Valkonen V,
WPI, 2001-2003/18/31.
DR P-PSDB; AAE00990.
XX

AA New DNA molecule encoding variant specific adrenoceptor protein with
PT deletion of specific amino acids located in the third intracellular loop
PT of the polypeptide, for treating vascular contraction of coronary
PT arteries.

Disclosure; Page 27-29; 37pp; English.

The present sequence is a gene encoding human α 1a2b-adrenoceptor (α 1a2b-AR) protein. α 1a2b-AR has a glutamic acid repeat element (amino acids 238-309) of 12 glutamates, in an acidic stretch of 18 amino acids (amino acids 234-311), located in the third intracellular loop of the receptor polypeptide. α 1a2b-AR gene is located on chromosome 2. α 1a2b-AR mediates many of the physiological effects of the catecholamines, norepinephrine and epinephrine. An antagonist of α 1a2b-adrenoceptor is useful for treating a mammal suffering from vascular contraction of coronary arteries and a disease involving vasopressor coronary heart disease (CHD), unstable chronic angina pectoris which is clinically expressed as Prinzmetal's variant form or acute myocardial infarction (AMI). α 1a2b-AR gene is used in gene therapy

Query Match 100.0%; Score 51; DB 5; Length 1353;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 51; Conservative 0

[illegible]

.....ADAGGAGGAGGAGGAGAGGTGT 930

RESULT 3
AD44389

AAU44389 standard; DNA; 1353 BP.
AAU44389;
13-DEC-2003 11:11

Human: hypertension, alpha-2A

Homo sapiens.
hypertension; hypotensive; gene; ds.
hypertension; alpha-2b-adrenoceptor; AR; antihypertensive;

Key	Location/Qualifiers
CDS	1..1353
	/*tag= a
	/product= "human alpha-op-4-actin"

MO200266617-A1.
29-AUG-2002.

13-FEB-2002; 2002MO-FI00113.
20-FEB-2001; 2001FI-00000323.

(JURI -) JURILAB LTD OY.
Salonen J,

DR WPI: 2002-667063/71.
DR P-PSDB; AAE26634.
XX
PT Detecting a risk of hypertension and targeting treatment in a subject by
PT determining the pattern of alleles encoding a variant alpha-2-
XX adrenoceptor.
XX
PS Disclosure; Page 27-29; 35pp; English.
XX
CC The invention relates to a method for detecting a risk of hypertension by
CC determining the pattern of alleles encoding a variant alpha-2B-
CC adrenoceptor (AR) protein. The methods and compositions of the invention
CC are useful for detecting risks and targeting treatment for hypertension.
CC The kit is also useful for selecting for clinical drug trials testing the
CC antihypertensive effect of compounds. The present sequence is human alpha
CC -2B-adrenoceptor gene
XX
SQ Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 6; Length 1353;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 51
DB 880 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 930

RESULT 4
ID AAQ14151 standard; DNA; 2064 BP.
XX
AC AAQ14151;
XX
DT 06-JAN-1992 (first entry)
XX
DE Human alpha 2 beta adrenergic receptor gene.
XX
KM Neurotransmission; adrenaline; epinephrine; NGC-alpha2beta; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 288..1752
FT /*tag= a
XX
XX US5053337-A.
XX
XX 01-OCT-1991.
XX
XX 30-OCT-1989; 89US-00428856.
XX
XX 30-OCT-1989; 89US-00428856.
XX
XX (NEUR-) NEUROGENETIC CORP.
XX
XX Weinshank RL, Hartig PR;
XX
XX WPI; 1991-310087/42.
XX
XX P-PSDB; AAR14149.
XX
XX Isolated DNA encoding human adrenergic receptor - for detecting nucleic
XX acids encoding alpha, 2-beta adrenergic receptor, for screening drugs.
XX
XX Claim 1; Fig 2; 15pp; English.
XX
XX Clone NGC-alpha2beta was isolated from a human spleen genomic library by
XX screening with a fragment of the human 5-HT1A receptor gene. The gene can
XX be used to express recombinant receptor protein which can be used to
XX produce antibodies for inhibition of receptor function
XX
SQ Sequence 2064 BP; 319 A; 696 C; 659 G; 390 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 2; Length 2064;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 51
DB 1278 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 1328

RESULT 5
ID AAT59499 standard; DNA; 2064 BP.
XX
AC AAT59499;
XX
DT 25-MAR-2003 (revised)
DT 06-MAY-1997 (first entry)
XX
XX
DE Human alpha-2B adrenergic receptor genomic DNA clone.
XX
XX Alpha-2B adrenergic receptor; adrenoceptor; adrenaline; epinephrine;
XX signal transduction; neurotransmitter; ligand; ss.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 288..1751
FT /*tag= a
XX
XX US5595880-A.
XX
XX 21-JAN-1997.
XX
XX 22-OCT-1992; 92US-00965040.
XX
XX 30-OCT-1989; 89US-00428856.
XX
XX 30-MAY-1991; 91US-00707604.
XX
XX (SYNA-) SYNAPTIC PHARM CORP.
XX
XX Hartig PR, Weinshank RL;
XX
XX WPI; 1997-107576/10.
XX
XX P-PSDB; AAM11804.
XX
XX Assay for alpha-2B adrenergic receptor ligands - using membranes of cells
XX expressing recombinant receptor.
XX
XX Disclosure; Fig 2A-E; 16pp; English.
XX
XX A genomic DNA clone (AAT59499) codes for human alpha-2B adrenergic
XX receptor (AAM11804), a member of the rhodopsin-like signal transducer
XX family. It was isolated from a human spleen genomic library in the lambda
XX vector Charon 28 by screening with a 1.6 kb fragment of the human 5-
XX hydroxytryptamine receptor gene. Plasmid pNC-alpha-2B comprising DNA
XX encoding the alpha-2B adrenoceptor is deposited as ATCC 68144. Vectors
XX have been adapted to allow prodn. of alpha-2B adrenoceptor in bacterial,
XX yeast or mammalian cells; transfected Ltk- cells, designated L-NGC-alpha-
XX 2B, are deposited as ATCC CRL 10275. Membranes of such cells can be used in
XX novel methods to identify drugs which specifically interact with, and
XX bind to, the alpha-2B adrenergic receptor. (Updated on 25-MAR-2003 to
XX correct PF field.)
XX
SQ Sequence 2064 BP; 319 A; 696 C; 659 G; 390 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 2; Length 2064;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 51
DB 1278 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 1328

RESULT 6
 ID ACAA56583
 ACAA56583 standard; cDNA; 2072 BP.
 ACN56583;
 06-JUN-2003 (first entry)
 Human signalling pathway polynucleotide probe SEQ ID NO 1181.
 Human; probe; ss: array element; Parkinson's disease;
 signalling pathway population; cancer; adenocarcinoma;
 immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
 Homo sapiens.
 US6500938-B1.
 31-DEC-2002.
 30-JAN-1998; 98US-00016434.
 30-JAN-1998; 98US-00016434.
 30-JAN-1998; 98US-00016434.
 (INCY-) INCYTE GENOMICS INC.
 Au-Young J, Seilhamer JJ;
 WPI; 2003-352189/33.
 Combination of polynucleotide probes, useful as array elements in a
 microarray for monitoring the expression of a number of target
 polynucleotides.
 Claim 1; SEQ ID NO 1181; 65pp; English.
 The invention relates to a combination which, comprises a number of
 polynucleotide probes comprising a sequence selected from one of the 1490
 sequences mentioned in the specification. The combination is useful as an
 array element in a microarray for monitoring the expression of a number
 of target polynucleotides. The microarray is particularly useful in the
 diagnosis and treatment of cancer and immunopathology and neuropathology.
 The microarray is useful in diagnostics and treatment regimens, drug
 discovery and development, toxicological and carcinogenicity studies,
 monitoring progression of diseases and for developing sophisticated
 profiles for the effects of currently available therapeutic drugs. The
 combination is also useful for purifying a subpopulation of mRNAs, CDNAs
 and genomic fragments and in research and diagnostic applications. The
 array can detect changes in expression in a large number of genes coding
 for different signalling pathway populations which can be used to diagnose
 various diseases including cancer e.g. adenocarcinoma and leukaemia,
 immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's
 disease and Parkinson's disease. The present sequence represents a polynucleotide
 probe of the invention. Note: The sequence data for this patent did not
 form part of the printed specification but was obtained in electronic
 format directly from USPTO at
 seqdata.uspto.gov/sequence.html?DocID=06500938B1
 Sequence 2072 BP; 316 A; 705 C; 660 G; 391 T; 0 U; 0 Other;
 Query Match 100.0%; Score 51; DB 7; Length 2072;
 Best Local Similarity 100.0%; Pred. No. 0.00056;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 51
 DB 1292 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 1342

ID AB242624 standard; DNA, 3274 BP.
 XX
 AC AB242624;
 XX
 DT 04-MAR-2003 (first entry)
 XX
 DE Human alpha 2b-adrenoceptor nucleotide SEQ ID NO:41.
 XX
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; inflammation; osteoarthritis; allergy
 KW osteoporosis; cardiomyopathy; infection; osteoarthritis; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW ulcer; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200261087-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 19-DEC-2001; 2001WO-US050107.
 XX
 PR 19-DEC-2000; 2000US-0257144P.
 XX
 PA 19-DEC-2000; 2000US-0257144P.
 XX
 PI (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX
 PI Burner GC, Roush CL, Brown JP;
 XX
 DR WPI: 2003-046718/04.
 XX
 DR P-PSDB; ABP81780.
 XX
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 PT autoimmune disease.
 PS
 PS Disclosure; Fig 1, 523pp; English.
 XX
 XX The present invention describes antigenic peptides (I) comprising: (a)
 XX any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 XX acids. Also described: (1) an assay for the detection of a particular G
 XX protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 XX and (2) an isolated antibody having high specificity and high affinity or
 XX avidity for a particular GPCR. (1) can be used as GPCR modulators and in
 XX gene therapy. The antigenic peptides for GPCRs are useful in detecting an
 XX antibody against a particular GPCR, and in the production of specific
 XX antibodies. The peptides and antibodies are also useful for detecting an
 XX presence or absence of corresponding GPCRs. The antigenic peptides for
 XX GPCR and antibodies are useful for diagnosing and designing drugs for
 XX treating immune-related diseases, growth-related diseases, cell
 XX regeneration-related diseases, growth-related diseases, cell
 XX disease, or autoimmune disease, immunological-related cell proliferative
 XX disease, or autoimmune disease, e.g. AIDS, Alzheimer's disease,
 XX osteoarthritis, osteoporosis, infection, osteoarthritis; allergy
 XX atherosclerosis; cardiomyopathy; inflammation; osteoarthritis; diabetes;
 XX graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 XX psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 XX mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 XX ulcer; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200261087-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 19-DEC-2001; 2001WO-US050107.
 XX
 PR 19-DEC-2000; 2000US-0257144P.
 XX
 PA 19-DEC-2000; 2000US-0257144P.
 XX
 PI (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX
 PI Burner GC, Roush CL, Brown JP;
 XX
 DR WPI: 2003-046718/04.
 XX
 DR P-PSDB; ABP81780.
 XX
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 PT autoimmune disease.
 PS
 PS Disclosure; Fig 1, 523pp; English.
 XX
 XX The present invention describes antigenic peptides (I) comprising: (a)
 XX any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 XX acids. Also described: (1) an assay for the detection of a particular G
 XX protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 XX and (2) an isolated antibody having high specificity and high affinity or
 XX avidity for a particular GPCR. (1) can be used as GPCR modulators and in
 XX gene therapy. The antigenic peptides for GPCRs are useful in detecting an
 XX antibody against a particular GPCR, and in the production of specific
 XX antibodies. The peptides and antibodies are also useful for detecting an
 XX presence or absence of corresponding GPCRs. The antigenic peptides for
 XX GPCR and antibodies are useful for diagnosing and designing drugs for
 XX treating immune-related diseases, growth-related diseases, cell
 XX regeneration-related diseases, growth-related diseases, cell
 XX disease, or autoimmune disease, immunological-related cell proliferative
 XX disease, or autoimmune disease, e.g. AIDS, Alzheimer's disease,
 XX osteoarthritis, osteoporosis, infection, osteoarthritis; allergy
 XX atherosclerosis; cardiomyopathy; inflammation; osteoarthritis; diabetes;
 XX graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 XX psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 XX mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 XX ulcer; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200261087-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 19-DEC-2001; 2001WO-US050107.
 XX
 PR 19-DEC-2000; 2000US-0257144P.
 XX
 PA 19-DEC-2000; 2000US-0257144P.
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 DR WPI: 2003-046718/04.
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 PS Disclosure; Fig 1, 523pp; English.
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 XX disease, or autoimmune disease, immunological-related cell proliferative
 XX disease, or autoimmune disease, e.g. AIDS, Alzheimer's disease,
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 XX atherosclerosis; cardiomyopathy; inflammation; osteoarthritis; diabetes;
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 XX psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 XX mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 XX ulcer; gene; ds.
 XX
 OS Homo sapiens.
 XX
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 PI (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX
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 XX treating immune-related diseases, growth-related diseases, cell
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 XX disease, or autoimmune disease, immunological-related cell proliferative
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 XX osteoarthritis, osteoporosis, infection, osteoarthritis; allergy
 XX atherosclerosis; cardiomyopathy; inflammation; osteoarthritis; diabetes;
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 XX psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 XX mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 XX ulcer; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200261087-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 19-DEC-2001; 2001WO-US050107.
 XX
 PR 19-DEC-2000; 2000US-0257144P.
 XX
 PA 19-DEC-2000; 2000US-0257144P.
 XX
 PI (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX
 PI Burner GC, Roush CL, Brown JP;
 XX
 DR WPI: 2003-046718/04.
 XX
 DR P-PSDB; ABP81780.
 XX
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 PT (GPCR), useful for diagnosing and designing drugs for treating conditions
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 PT autoimmune disease.
 PS
 PS Disclosure; Fig 1, 523pp; English.
 XX
 XX The present invention describes antigenic peptides (I) comprising: (a)
 XX any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 XX acids. Also described: (1) an assay for the detection of a particular G
 XX protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 XX and (2) an isolated antibody having high specificity and high affinity or
 XX avidity for a particular GPCR. (1) can be used as GPCR modulators and in
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 XX antibody against a particular GPCR, and in the production of specific
 XX antibodies. The peptides and antibodies are also useful for detecting an
 XX presence or absence of corresponding GPCRs. The antigenic peptides for
 XX GPCR and antibodies are useful for diagnosing and designing drugs for
 XX treating immune-related diseases, growth-related diseases, cell
 XX regeneration-related diseases, growth-related diseases, cell
 XX disease, or autoimmune disease, immunological-related cell proliferative


```
DR      WPI; 2003-587068/55.
XX
PT      New recombinant nucleic acid encoding carcinoma associated protein,
FT      useful for preparing compositions for treating carcinomas.
XX
PS      Claim 1; SEQ ID NO 1583; 245pp; English.
CC      The invention relates to recombinant carcinoma associated (CA) nucleic
CC      acid sequences from mouse and human (ADA01482-DA03094), and to
CC      recombinant carcinoma associated proteins (CAP) encoded by them. The
CC      invention also encompasses expressed vectors and host cells comprising a
CC      CA nucleic acid, a polypeptide (especially an antibody) that specifically
CC      binds to the protein, and a bioclip comprising CA nucleic acid or
CC      fragments thereof. The sequences of the invention were identified using
CC      oncogenic retroviruses, which insert into the genome of the host organism
CC      at random. Many of these do not carry transduced host oncogenes or
CC      pathogenic trans-acting viral genes, meaning that cancer incidence is a
CC      direct consequence of the effects of proviral integration into host
CC      protooncogenes. The CA nucleic acid sequences can be used to diagnose
CC      carcinoma (especially breast cancer, prostate cancer, lymphoma or
CC      leukemia) or a propensity to carcinoma by determination of the sequence
CC      of a CA gene, or by determination of CA gene expression in particular
CC      tissues. CA nucleic acids, proteins and antibodies are also useful as
CC      therapeutic agents and in screening and evaluating drug candidates. The
CC      present sequence represents a specifically claimed murine CA nucleic acid
CC      sequence of the invention. Note: The complete sequence data for this
CC      patent did not form part of the printed specification, but was obtained
CC      in electronic format directly from WIPO at
XX      ftp.wipo.int/pub/published_pct_sequences.
SQ      Sequence 68233 BP; 18767 A; 14103 C; 14729 G; 20634 T; 0 U; 0 Other;
Query Match          81.6%; Score 41.6; DB 8; Length 68233;
Best Local Similarity 91.7%; Pred. No. 0.12;
Matches    44; Conservative   0; Mismatches     4; Indels    0; Gaps    0
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Db       66088 GAGGAGGAGAACGAAAGAGAGAGAGAGGAGGAGGAGGAGGAGAGAG 66041
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ADB72803/C
ID      ADB72803 standard; DNA; 68233 BP.
XX
XX      ADB72803;
AC      AC
XX
DT      04-DEC-2003 (first entry)
XX
DE      Mouse Ppj3c gene.
XX
KW      mouse; dg; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;
KW      cancer; neoplasm; adenocarcinoma; sarcoma; gene.
OS      Mus sp.
XX
PN      WO2003008583-A2.
XX
PD      30-JAN-2003.
XX
PF      26-DEC-2001; 2001WO-US051291.
XX
PR      02-MAR-2001; 2001US-00798586.
PR      23-OCT-2001; 2001US-00004113.
PR      08-NOV-2001; 2001US-00052482.
PR      30-NOV-2001; 2001US-00997722.
PR      20-DEC-2001; 2001US-00034650.
XX
PA      (SAGR-) SAGRES DISCOVERY.
XX
FI      Morris DW, Engelhard EK;
OR      WPI; 2003-239337/23.
```

PT	New recombinant nucleic acid, useful for treating carcinomas, lymphomas,
FT	cancers, neoplasm, adenocarcinoma, or sarcomas.
XX	
XX	Claim 1; SEQ ID NO 631; 2304pp; English.
CC	The invention relates to a novel recombinant nucleic acid comprising a
CC	nucleotide sequence selected from any of the 660 sequences fully defined
CC	in the specification. A polynucleotide of the invention has cytosatic
CC	activity, and may have a use in gene therapy, or in a vaccine. The
CC	recombinant nucleic acids and polypeptides are useful for treating
CC	carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and
CC	sarcomas. The present sequence represents a mouse gene of the invention.
XX	
XX	Sequence 68233 BP; 18767 A; 14103 C; 14729 G; 20634 T; 0 U; 0 Other;
SQ	
	Query Match 81.6%; Score 41.6; DB 9; Length 68233;
	Best Local Similarity 91.7%; Pred. No. 0.12;
	Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY	
Db	1 GAGGATGAAGCTGAAGAGAGAAAGAGGAGAGAGAGAGAGAGAGAG 48 66088 GAGGAGGAGAACAAGAAAGAGAGAAAGAGAGAGAGAGAGAGAGAG 66041
RESULT 14	
ALJ8337/C	
ID	ALJ8337 standard; DNA; 215980 BP.
AC	ALJ8337.
XX	
XX	15-AUG-2002 (first entry)
DE	
XX	Complementary strand of a genomic sequence encoding a mouse NGR3.
XX	
KM	Cerebroprotective; neuroprotective; cyrostatic; Nogo receptor homologue;
KM	NGR2; NGR3; axonal growth; central nervous system; CNS; cerebral injury;
KM	spinal cord injury; stroke; demyelinating disease; multiple sclerosis;
KM	monophasic demyelination; encephalomyelitis; Marchiafava-Bignami disease;
KM	multifocal leukoencephalopathy; panencephalitis; Spongy degeneration;
KM	Alexander's disease; Canavan's disease; metachromatic leukodystrophy;
KM	Krabbe's disease; immune; bait protein; genetic mapping; gene therapy;
KW	transgenic animal; unregulated cellular growth; cancer; tumour; mouse;
KM	murine; ds.
OS	Mus sp.
XX	
XX	WO200229059-A2.
PN	
XX	11-APR-2002.
PD	
PF	06-OCT-2001; 2001WO-US031488.
XX	
XX	06-OCT-2000; 2000US-0238361P.
DR	
XX	(UYTA) UNIT YALE.
PA	(BIOJ) BIOGEN INC.
XX	
PI	Strittmatter SM, Cate RL, Sah DWY;
XX	
XX	WPI; 2002-416677/44.
XX	
PT	Novel Nogo receptor homolog polypeptide, NGR2 or NGR3, useful for
PT	treating central nervous system disorder, cerebral injury, spinal cord
PT	injury, stroke, and demyelinating diseases.
XX	
XX	Example 16; Page 219-275; 277pp; English.
CC	The invention relates to a Nogo receptor homologue polypeptide, NGR2 or
CC	NGR3, comprising a 50 amino acid LRRCR sequence, a 284 amino acid NTLRCTR
CC	sequence, or a 420, 461 or 392 amino acid sequence, all given in the
CC	specification. The NGR3 protein or its binding antibody is useful for
CC	decreasing inhibition of axonal growth of a central nervous system (CNS)

Query Match	81.6%	Score 41.6;	DB 6;	length 215980;
Best local Similarity	91.7%	Pred. No. 0.13;		
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XY	

DT 21-NOV-2002 (First entry)
XX

S. cerevisiae BAX-associated cDNA fragment SEQ ID 261..

neurodegeneration; cell death; ss.

Saccharomyces cerevisiae.

WO200264766-A2

22-AUG-2002

21-DEC-2001; 2001WO-EP015398

22-DEC-2000; 2000EP-00870318.

09-JAN-2001; 2001EP-00870003.

(JANC) JANSSEN PHARM NV.

Contreras RH, Eberhardt I, Luyten WHML, Reekmans RJ, I

WPI; 2002-667002/71.
B-BENB: 1BCC031EC

New! at our

medicament for treating, preventing and/or alleviating yeast or fungal infections or proliferative disorders, or for preventing apoptosis in certain diseases.

Claim 36; Fig 1; 344pp; English.

CC This invention describes a novel nucleic acid representing a synthetic
CC Bax gene. The Bax gene of the invention is useful for identifying
CC Bax-resistant yeast or fungi, identifying, or obtaining and identifying
CC Candida spp. sequences that are differentially expressed in a pathway
CC eventually leading to programmed cell death or identifying inhibitors or
CC inhibitor sequences of Bax-induced cell death. The products of the
CC invention have cytostatic, fungicidal, immunosuppressive, virucidal and
CC virotoxic activity and can be used in vaccines or for gene therapy. The
CC isolated nucleic acids, polypeptides, pharmaceutical compositions,
CC antisense molecules and antibodies are useful as medicaments or in
CC preparing a medicament for treating, preventing and/or alleviating
CC diseases associated with yeast or fungi or proliferative disorders, such
CC as cancer, or for preventing apoptosis in certain diseases. The compounds
CC or polypeptides, or the genetically modified organism are useful for
CC preparing a medicament for modifying the endogenous flora of humans and
CC other mammals. The vaccine is useful for immunizing against yeast or
CC fungal infections. Apoptosis-related diseases include autoimmune disease,
CC ischaemia, diseases related with viral infections or neurodegenerations.
CC This sequence represents a polynucleotide associated with the Bax gene
CC described in the disclosure of the invention
XX

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SV sequence 1721 BP; 501 A; 400 C; 341 G; 479 T; 0 U; 0 Other;
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Best Local Similarity 91.5%; Pred. No. 0.2;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0

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[illegible]

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Search completed: March 2, 2004, 05:39:00
Job time : 267.5 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2004, 05:39:14 ; Search time 60 Seconds

(without alignments)
471.708 Million cell updates/sec

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Sequence: 1 gagagatgaagctgaagagga.....agagagagaggaagatgc 51

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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25: /cgn2_6/ptodata/2/ina/6W_COMB.seq:*

26: /cgn2_6/ptodata/2/ina/6X_COMB.seq:*

27: /cgn2_6/ptodata/2/ina/6Y_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	2072	4	US-09-016-434-1181
2	40	78.4	2663	4	US-09-533-029-47
3	38.4	75.3	636	4	US-09-702-705-1668
4	38.4	75.3	636	4	US-09-736-457-1668
5	38.4	75.3	636	4	US-09-614-124B-1668
6	38.4	75.3	636	4	US-09-671-325-1668
7	38.4	75.3	650	4	US-09-328-111-333
8	37.4	73.3	1194	4	US-09-220-132-31
9	36.8	72.2	58	3	US-08-860-038-15
10	36.8	72.2	58	3	US-08-860-038-15
11	36.8	72.2	58	3	US-08-860-038-15
12	36.8	72.2	58	3	US-08-860-038-15
13	36.8	72.2	58	3	US-08-860-038-15
14	36.8	72.2	58	3	US-08-860-038-15
15	36.8	72.2	58	3	US-08-860-038-15
16	36.8	72.2	58	3	US-08-860-038-15
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18	36.8	72.2	58	3	US-08-860-038-15
19	36.8	72.2	58	3	US-08-860-038-15
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21	36.8	72.2	58	3	US-08-860-038-15
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23	36.8	72.2	58	3	US-08-860-038-15
24	36.8	72.2	58	3	US-08-860-038-15
25	36.8	72.2	58	3	US-08-860-038-15
26	36.8	72.2	58	3	US-08-860-038-15
27	36.8	72.2	58	3	US-08-860-038-15

ALIGNMENTS

28	36.8	72.2	5573	4	US-09-418-710-30	Sequence 30, Appl
29	36.8	72.2	6114	4	US-09-495-714C-5	Sequence 5, Appl
30	36.8	72.2	45676	3	US-09-356-952-12	Sequence 12, Appl
31	36.8	72.2	51259	3	US-08-781-891-209	Sequence 209, Appl
32	36.8	72.2	51259	4	US-09-618-166-209	Sequence 209, Appl
33	36.4	71.4	2609	3	US-09-141-212-7	Sequence 7, Appl
34	36.4	71.4	2609	3	US-09-561-138-7	Sequence 7, Appl
35	36.4	71.4	2669	3	US-09-141-212-9	Sequence 9, Appl
36	36.4	71.4	2669	3	US-09-561-138-9	Sequence 9, Appl
37	36.4	71.4	2693	3	US-09-141-212-5	Sequence 5, Appl
38	36.4	71.4	2693	3	US-09-561-138-5	Sequence 5, Appl
39	36.4	71.4	3255	2	US-08-916-917-11	Sequence 11, Appl
40	36.4	71.4	3255	2	US-09-225-170-11	Sequence 11, Appl
41	36.4	71.4	3630	3	US-09-378-255-5	Sequence 5, Appl
42	36.4	71.4	3630	3	US-09-141-212-1	Sequence 1, Appl
43	36.4	71.4	3630	3	US-09-141-212-3	Sequence 3, Appl
44	36.4	71.4	3630	3	US-09-552-351-3	Sequence 3, Appl
45	36.4	71.4	3630	3	US-09-251-372-5	Sequence 5, Appl

RESULT 1
US-09-016-434-1181
Sequence 1181, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1181:
SEQUENCE CHARACTERISTICS:
LENGTH: 2072 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 918197
US-09-016-434-1181
Query Match: 100.0%; Score 51; DB 4; Length 2072;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;

;; TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN
;; FILE REFERENCE: 03804.0138-01
;; CURRENT APPLICATION NUMBER: US/09/580,923
;; CURRENT FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 08/860,038
;; PRIOR FILING DATE: 1997-06-09
;; PRIOR APPLICATION NUMBER: PCT/FR95/01468
;; PRIOR FILING DATE: 1995-11-08
;; NUMBER OF SEQ ID NOS: 36
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 16
;; LENGTH: 58
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:
US-09-580-923-16

Query Match 72.2%; Score 36.8; DB 4; Length 58;
Best Local Similarity 85.4%; Pred. No. 0.099;
Matches 41; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 48
Db 56 GAGGAG 9

RESULT 13
US-09-894-998A-34/C
Sequence 34, Application US/09894998A
Patent No. 6537555

;; GENERAL INFORMATION:
;; APPLICANT: Hosken, Nancy Ann
;; APPLICANT: Craig H. Day
;; APPLICANT: David C. Dillon
;; APPLICANT: McGowan, Patrick
;; APPLICANT: Sleeth, Paul R.
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
;; TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
;; FILE REFERENCE: 210121.538
;; CURRENT APPLICATION NUMBER: US/09/894,998A
;; CURRENT FILING DATE: 2001-06-28
;; NUMBER OF SEQ ID NOS: 64
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 34
;; LENGTH: 661
;; TYPE: DNA
;; ORGANISM: HSV-2
US-09-894-998A-34

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Best Local Similarity 85.4%; Pred. No. 0.12;
Matches 41; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 48
Db 51 GAGGAG 4

RESULT 14
US-09-163-285-3
Sequence 3, Application US/09163285
Patent No. 6204013

;; GENERAL INFORMATION:
;; APPLICANT: Knodadoust, Mehran
;; TITLE OF INVENTION: NOVEL MSP-5 PROTEIN AND NUCLEIC ACID MOLECULES
;; TITLE OF INVENTION: AND USES THEREOF
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: LAHIVE & COCKFIELD, LLP
;; STREET: 28 State Street

;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: USA
;; ZIP: 02109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC Compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/163,285
;; FILING DATE:

;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/090,398
;; FILING DATE: June 24, 1998
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mandragoras, Amy E.
;; REGISTRATION NUMBER: 36,207
;; REFERENCE/DOCKET NUMBER: MNI-049
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617)227-7400
;; TELEFAX: (617)742-4214
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 744 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..744

US-09-163-285-3

Query Match 72.2%; Score 36.8; DB 3; Length 744;
Best Local Similarity 85.4%; Pred. No. 0.12;
Matches 41; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 48
Db 628 GAGGAG 675

RESULT 15
US-09-163-285-1

;; Sequence 1, Application US/09163285
;; Patent No. 6204013
;; GENERAL INFORMATION:
;; APPLICANT: Knodadoust, Mehran
;; TITLE OF INVENTION: NOVEL MSP-5 PROTEIN AND NUCLEIC ACID MOLECULES
;; TITLE OF INVENTION: AND USES THEREOF
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: LAHIVE & COCKFIELD, LLP
;; STREET: 28 State Street
;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: USA
;; ZIP: 02109

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC Compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/163,285
;; FILING DATE:

;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/090,398
;; FILING DATE: June 24, 1998
;; ATTORNEY/AGENT INFORMATION:

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OM nucleic - nucleic search, using NW model

Run on: March 2, 2004, 10:12:50 ; Search time 140 Seconds

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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	51	100.0	1353	14	US-10-077-870-3
3	51	100.0	1353	14	US-10-001-073-1
4	51	100.0	2072	15	US-10-305-720-1181
5	51	100.0	3274	15	US-10-225-567A-41
6	41.6	81.6	68233	15	US-10-034-650-31
7	41.6	81.6	215980	10	US-09-972-546-16
8	40.2	78.8	1344	9	US-09-825-923-1
9	40.2	78.8	1344	14	US-10-077-870-1
10	40	78.4	223	9	US-09-728-444-146
11	40	78.4	234	9	US-09-728-446-1420
12	40	78.4	330	9	US-09-728-444-124
13	40	78.4	642	12	US-10-425-114-10223
14	40	78.4	1173	15	US-10-161-927-81
15	40	78.4	1178	15	US-10-161-927-83

16	40	78.4	1290	12	US-10-424-599-47976	Sequence 47976, A
17	40	78.4	1433	12	US-10-425-114-19415	Sequence 19415, A
18	40	78.4	2367	14	US-10-128-714-6204	Sequence 6204, Ap
19	40	78.4	2367	14	US-10-128-714-7204	Sequence 7204, Ap
20	40	78.4	2663	10	US-09-533-029-47	Sequence 47, Appl
21	40	78.4	2663	10	US-09-934-455-177	Sequence 45, Appl
22	40	78.4	2663	15	US-10-225-068-65	Sequence 65, Appl
23	40	78.4	2663	15	US-10-302-267-45	Sequence 45, Appl
24	40	78.4	2663	15	US-10-374-780A-229	Sequence 229, App
25	40	78.4	4238	14	US-10-128-714-5204	Sequence 5204, Ap
26	40	78.4	4367	14	US-10-128-714-5204	Sequence 17979, A
27	39	76.5	191	14	US-10-029-386-17979	Sequence 18355, A
28	39	76.5	423	9	US-09-864-761-18355	Sequence 1597, Ap
29	39	76.5	487	9	US-10-029-386-4279	Sequence 4279, Ap
30	39	76.5	543	14	US-10-211-859-4	Sequence 115, App
31	39	76.5	1788	10	US-09-893-519A-115	Sequence 216, App
32	39	76.5	1977	14	US-10-102-806-216	Sequence 97636, A
33	39	76.5	2134	15	US-10-027-632-97636	Sequence 103743, A
34	39	76.5	2480	15	US-10-027-632-103743	Sequence 1892, Ap
35	39	76.5	2480	15	US-10-027-632-11750	Sequence 1892, Ap
36	39	76.5	3769	14	US-10-175-523-184	Sequence 1892, Ap
37	39	76.5	3769	14	US-10-175-523-184	Sequence 1892, Ap
38	39	76.5	23130	9	US-09-764-869-1892	Sequence 1892, Ap
39	39	76.5	23130	14	US-10-091-504-1892	Sequence 1892, Ap
40	39	76.5	23130	15	US-10-227-577-1892	Sequence 1892, Ap
41	39	76.5	33226	9	US-09-818-264-3	Sequence 3, Appl
42	39	76.5	106664	14	US-10-175-523-97	Sequence 97, Appl
43	39	76.5	6222	15	US-10-120-988-114	Sequence 114, Appl
44	38.6	75.7	6452	9	US-09-954-456-308	Sequence 308, App
45	38.4	75.3	54	15	US-10-418-182-296	Sequence 296, App

ALIGNMENTS

RESULT 1

US-09-825-923-3

Sequence 3, Application US/09825923

Patent No. US20010016338A1

GENERAL INFORMATION:

APPLICANT: Snapir, Amir

APPLICANT: Heimonen, Paula

APPLICANT: Alhopuro, Pia

APPLICANT: Karvonen, Matti

APPLICANT: Koulou, Markku

APPLICANT: Pesonen, Ulla-Mari

APPLICANT: Scheinin, Mika

APPLICANT: Salonen, Jukka T

APPLICANT: Tuomainen, Tomi-Pekka

APPLICANT: Lakka, Timo A

APPLICANT: Nyyssänen, Kristiina

APPLICANT: Salonen, Riitta

APPLICANT: Kauppinen, Jussi

APPLICANT: Valkonen, Veli-Pekka

TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor

FILE REFERENCE: Alpha-2B-AR variant

CURRENT APPLICATION NUMBER: US/09/825,923

CURRENT FILING DATE: 2001-04-05

PRIOR APPLICATION NUMBER: 09/422,985

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 3

LENGTH: 1353

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(1350)

OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor

OTHER INFORMATION: protein

US-09-825-923-3

	Query Match	Similarity	100.0%	Score 51	DB 9	Length 1553
	Best Local	Similarity	100.0%	Pred. No.	976	0
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				Gaps	0	
QY	1	GAGATGTAAGCTGAAGACGAGAAGAGAGAGAGAGAGAGAAAGACTGT	51			
Dd	880	GAGATGTAAGCTGAAGACGAGAAGAGAGAGAGAGAGAGAAAGACTGT	930			

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RESULT 2
US-10-077-870-3
; Sequence 3, Application US/10077870
; Publication No. US20030003470A1
; GENERAL INFORMATION:
; APPLICANT: Salonen, Jukka T
; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
; FILE REFERENCE: 0933-0183P
; CURRENT APPLICATION NUMBER: US/10/077,870
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: FI 20010323
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1350)
; OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor protein
;S-10-077-870-3

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QY

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Dd 880 GAGCATTGAAGTGAAGAAGAGAGAGAGAGAGAAAGACTGT 930

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RESULT 3
US-10-001-073-1
; Sequence 1, Application US/10001073
; Publication No. US20030113725A1
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; APPLICANT: Small, Kirsten
; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
; FILE REFERENCE: 13073-PCT
; CURRENT APPLICATION NUMBER: US/10/001,073
; CURRENT FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1353
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-001-073-1

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Query Match	100.0%	Score 51;	DB 14;	Length 1353;
Best Local Similarity	100.0%	Pred. No. 97e-06;		
Matches	51;	Conservative 0;	Mismatches 0;	Gaps 0;
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Dd	880	GAGGATGAAAGCTTGAAAGGAGGAAGGAGGAGGAGGAAGAGTGT	930	

RESULT 4
US-10-305-720-1181

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: Sequence 1181: Application US/10305720
: Publication No. US20040010136A1
: GENERAL INFORMATION:
: APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
: TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
: FILE REFERENCE: EP-0002-1 CON
: CURRENT APPLICATION NUMBER: US/10/305,720
: PRIORITY FILING DATE: 2002-11-26
: PRIOR APPLICATION NUMBER: 09/016,434
: NUMBER OF SEQ ID NOS: 1490
: SOFTWARE: PERL Program
: SEQ ID NO 1181
: LENGTH: 2072
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: GenBank ID NO. US20040010136A1 5178197
: US-10-305-720-1181

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RESULT 5
US-10-225-567A-41
; Sequence 41, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
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; LENGTH: 3274
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-225-567A-41

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RESULT 6
US-10-034-650-31/C
Sequence 31, Application US/10034650
Publication NO. US20030216558A1
GENERAL INFORMATION:
APPLICANT: Morris, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITILE OF INVENTION: CANCER
FILE REFERENCE: 529452000128
CURRENT APPLICATION NUMBER: US/10/034,650

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CURRENT FILING DATE: 2002-05-21

RESULT 11
 US-09-728-446-1420/c
 ; Sequence 1420, Application US/09728446
 ; Patent No. US20020081668A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: No. US20020081668A1 Murine Polynucleotide Sequences
 ; TITLE OF INVENTION: and Mutant Cells and Mutant Animals Defined Thereby
 ; FILE REFERENCE: LEX-0101-USA
 ; CURRENT APPLICATION NUMBER: US/09/728,446
 ; CURRENT FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: US 60/166,270

RESULT 13
 US-10-425-114-10213
 : Sequence 10213, Application US/10425114
 : Publication No. US20040034888A1
 : GENERAL INFORMATION:
 : APPLICANT: Liu, Jingdong
 : APPLICANT: Zhou, Yihua
 : APPLICANT: Kovalic, David K.
 : APPLICANT: Screen, Steven B
 : APPLICANT: Tabaska, Jack E
 : APPLICANT: Cao, Yongwei
 : TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 : TITLE OR INVENTION: Plants and Uses Thereof for Plant Improvement
 : FILE REFERENCE: 38-21(5313)B
 : CURRENT APPLICATION NUMBER: US/10/425.114

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	51	100.0	69	29	US-09-692-077D-24	Sequence 24, App
2	51	100.0	63	43	US-10-001-073A-54	Sequence 54, App
C 3	51	100.0	481	72	US-60-164-763-274	Sequence 274, App
C 4	51	100.0	481	72	US-60-169-842-1935	Sequence 1935, App
C 5	51	100.0	481	73	US-60-170-346-61	Sequence 61, App
6	51	100.0	356	31	US-09-726-174-3537	Sequence 3537, App
7	51	100.0	359	72	US-60-160-189-1492	Sequence 1492, App
8	51	100.0	569	72	US-60-160-180-020-231	Sequence 231, App
9	51	100.0	569	72	US-60-160-202-659	Sequence 659, App
10	51	100.0	569	72	US-60-169-840-3708	Sequence 3708, App
11	51	100.0	569	72	US-60-168-841-1172	Sequence 1172, App
12	51	100.0	569	72	US-60-163-842-2193	Sequence 2193, App
13	51	100.0	569	72	US-60-169-867-3351	Sequence 3351, App
14	51	100.0	1353	20	US-09-422-985-3	Sequence 3, App
15	51	100.0	1353	29	US-09-692-077B-1	Sequence 1, App
16	51	100.0	1353	29	US-09-692-077D-1	Sequence 1, App
17	51	100.0	1353	33	US-09-825-923-3	Sequence 3, App
18	51	100.0	1353	43	US-10-001-073-1	Sequence 1, App
19	51	100.0	1353	43	US-10-001-073A-1	Sequence 1, App
20	51	100.0	1353	44	US-10-077-870-3	Sequence 3, App
21	51	100.0	1353	44	US-10-170-225-40719	Sequence 40719, App
22	51	100.0	1353	102	US-60-453-050-6437	Sequence 6437, App
23	51	100.0	1353	102	US-60-453-135-6437	Sequence 6437, App
24	51	100.0	1353	103	US-60-466-412-6437	Sequence 412, App
25	51	100.0	1825	39	US-09-949-004-175	Sequence 175, App
26	51	100.0	2072	49	US-10-305-120-1181	Sequence 1181, App
27	51	100.0	3774	47	US-10-225-567A-41	Sequence 41, App
28	51	100.0	3655	107	US-60-500-315-890	Sequence 890, App
29	51	100.0	3691	107	US-60-500-315-891	Sequence 891, App
30	51	100.0	4050	76	US-60-207-360-68	Sequence 68, App
31	51	100.0	4050	76	US-60-207-360-110	Sequence 110, App
32	51	100.0	4050	76	US-60-207-360-111	Sequence 111, App
33	51	100.0	4050	76	US-60-207-360-112	Sequence 112, App
34	51	100.0	4050	76	US-60-207-360-113	Sequence 113, App
35	51	100.0	4050	76	US-60-207-360-114	Sequence 114, App
36	51	100.0	4050	76	US-60-207-360-115	Sequence 115, App
37	51	100.0	4050	76	US-60-207-360-116	Sequence 116, App
38	51	100.0	4050	76	US-60-207-360-117	Sequence 117, App
39	51	100.0	4050	76	US-60-207-360-118	Sequence 118, App
40	51	100.0	5259	78	US-60-229-515-121	Sequence 121, App
41	51	100.0	5349	81	US-60-245-225-211	Sequence 211, App
42	51	100.0	6786	81	US-60-248-505-165	Sequence 165, App
43	51	100.0	6806	39	US-09-949-004-641	Sequence 641, App
44	51	100.0	9842	73	US-60-172-372-2914	Sequence 2914, App
45	51	100.0	9842	89	US-60-224-185-27415	Sequence 27415, App

ALIGNMENTS

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RESULT 1
US-09-692-077D-24
; Sequence 24, Application US/09692077D
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; APPLICANT: Small, Kersten M.
; TITLE OF INVENTION: Alpha-2B-Adrenergic Receptor Polymorphisms
; FILE REFERENCE: 10738-43
; CURRENT APPLICATION NUMBER: US/09/692,077D
; CURRENT FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 69
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-692-077D-24

Query Match          100.0%; Score 51; DB 29; Length 69;

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best local similarity 100.0%;  Pred. No. 0.15;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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[illegible]

RESULT 2
ITS-10-00

sequence 54, Application US/10001073A

APPLICANT: Small, Kersten M.

FILE OF INVENTION: Alpha-2 Adrenergic Receptor Polymorphisms
FILE REFERENCE: 10738-42

CURRENT APPLICATION NUMBER: US/10/001,073A
CURRENT FILING DATE: 2001-11-01

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' NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.2

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LENGTH: 65

ORGANISM: *Homo sapiens*

US-10-001-073A-54

Query Match	Score	DB	Length
100.0%;	51;	43;	69;

Matches	51;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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1 GAGGATGACCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGTGT 51

DB 12 GAGGATGAACCTGAAGAAGAGGAGGAGGAGGAGGAGGAGGAGACTGT 62

RESULT 3

Sequence 274, Application US/60164763

APPLICANT: Bonazzi, Vivien

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN GPCR P

; CURRENT APPLICATION NUMBER: US/60/164,763

NUMBER OF SEQ ID NOS: 1154

; SEQ ID NO 274

TYPE: DNA

US-60-164-763-274

Query Match	100.0%;	Score 51;	DB 72;	Length 481;
Best Local Similarity	100.0%			

Matches	51;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
---------	-----	--------------	----	------------	----	--------	----	------	----

1 GAGGATGAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGT 51

227 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGT 177

RESULT 4

Sequence 1935, Application NS/60169842

APPLICANT: Bonazzi

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN GPCR PROTEIN, NUCLEIC

CURRENT APPLICATION NUMBER: US/60/169,842

NUMBER OF SEQ ID NOS: 5232

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1935
LENGTH: 481
TYPE: DNA
ORGANISM: Human
US-60-169-842-1935

Query Match 100.0%; Score 51; DB 72; Length 481;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGTGT 51
Db 227 GAGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGTGT 177

RESULT 5
US-60-170-346-61/c
Sequence 61, Application US/60170346
GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
TITLE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, NUCLEIC
FILE REFERENCE: CL000147
CURRENT APPLICATION NUMBER: US/60/170,346
CURRENT FILING DATE: 1999-12-13
NUMBER OF SEQ ID NOS: 2600
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 61
LENGTH: 481
TYPE: DNA
ORGANISM: Human
US-60-170-346-61

Query Match 100.0%; Score 51; DB 73; Length 481;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGTGT 51
Db 227 GAGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGTGT 177

RESULT 6
US-09-726-174-3537
Sequence 3537, Application US/09726174
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
FILE REFERENCE: 1600.2012-001
CURRENT APPLICATION NUMBER: US/09/726,174
CURRENT FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 60/167,857
PRIOR FILING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 5942
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3537
LENGTH: 516
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(516)
OTHER INFORMATION: n = A,T,C or G
US-09-726-174-3537

Query Match 100.0%; Score 51; DB 31; Length 516;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGTGT 51

Db 243 GAGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGTGT 293

RESULT 7
US-60-160-189-1492
Sequence 1492, Application US/60160189
GENERAL INFORMATION:
APPLICANT: BONAZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS
FILE REFERENCE: CL000112
CURRENT APPLICATION NUMBER: US/60/160,189
CURRENT FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 10162
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1492
LENGTH: 569
TYPE: DNA
ORGANISM: HUMAN
US-60-160-189-1492

Query Match 100.0%; Score 51; DB 72; Length 569;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGTGT 51
Db 24 GAGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGTGT 74

RESULT 8
US-60-160-190-231
Sequence 231, Application US/60160190
GENERAL INFORMATION:
APPLICANT: BONAZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN ION CHANNEL PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN ION CHANNEL PROTEINS
FILE REFERENCE: CL000115
CURRENT APPLICATION NUMBER: US/60/160,190
CURRENT FILING DATE: 1998-10-19
NUMBER OF SEQ ID NOS: 2384
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 231
LENGTH: 569
TYPE: DNA
ORGANISM: HUMAN
US-60-160-190-231

Query Match 100.0%; Score 51; DB 72; Length 569;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGTGT 51
Db 24 GAGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGTGT 74

RESULT 9
US-60-160-202-659
Sequence 659, Application US/60160202
GENERAL INFORMATION:
APPLICANT: BONAZZI, VIVIEN
TITLE OF INVENTION: ISOLATED HUMAN GPCR PROTEIN, NUCLEIC
FILE REFERENCE: CL000114
CURRENT APPLICATION NUMBER: US/60/160,202
CURRENT FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 4392
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 659

CURRENT APPLICATION NUMBER: US/09/422,985
CURRENT FILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 1353
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1350)
OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor
OTHER INFORMATION: protein
US-09-422-985-3

Query Match 100.0%; Score 51; DB 20; Length 1353;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGT 51
|||||
DB 880 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGT 930
|||||

RESULT 15
US-09-692-077B-1
Sequence 1, Application US/09692077B
GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
TITLE OF INVENTION: Alpha-2B-adrenergic receptor polymorphisms
FILE REFERENCE: Sequences 1-22
CURRENT APPLICATION NUMBER: US/09/692,077B
CURRENT FILING DATE: 2000-10-19
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1353
TYPE: DNA
ORGANISM: Homo sapiens
US-09-692-077B-1

Query Match 100.0%; Score 51; DB 29; Length 1353;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGT 51
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DB 880 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGT 930
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Search completed: March 2, 2004, 11:49:23
Job time : 2893 secs

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CURRENT FILING DATE: 2003-08-18
PRIOR APPLICATION NUMBER: US/09/957,956
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 60/234,422
PRIOR FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 45980
TYPE: DNA
ORGANISM: Homo sapiens
US-10-642-946-6

Query Match      73.3%   Score 37.4; DB 6; Length 45980;
Best Local Similarity 87.2%; Pred.No.0.033;
Matches 41; Conservative 0; Mismatches 6; Indels 0; Gaps 0.

Oy          1 GAGGATGAAGCTGAAGAAGAGAGAGAGAGAGAGAGAGA 47
Db          3845 GAGCAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAA 3891

RESULT 8
PCT-US03-32805-1
Sequence 1, Application PC/TUS0332805
GENERAL INFORMATION:
APPLICANT: decode genetics ehf.
APPLICANT: Helgadottir, Anna
APPLICANT: Gulcher, Jeffrey R.
APPLICANT: Manolescu, Andrei
TITLE OF INVENTION: Susceptibility Gene for Myocardial
TITLE OR INVENTION: Infarction
FILE REFERENCE: 2345.2048002
CURRENT APPLICATION NUMBER: PCT/US03/32805
CURRENT FILING DATE: 2003-10-16
PRIOR APPLICATION NUMBER: 60/419,432
PRIOR FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 535
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 398800
TYPE: DNA
ORGANISM: homo sapiens
FEATURES:
NAME/KEY: misc_feature
LOCATION: (70677)...(70776)
OTHER INFORMATION: n = A,T,C or G
FEATURE:
NAME/KEY: misc_feature
LOCATION: (154988)...(155087)
OTHER INFORMATION: n = A,T,C or G
FEATURE:
NAME/KEY: misc_feature
LOCATION: 248521
OTHER INFORMATION: n = A,T,C or G
FEATURE:
NAME/KEY: misc_feature
LOCATION: (263991)...(270091)
OTHER INFORMATION: n = A,T,C or G
FEATURE:
NAME/KEY: misc_feature
LOCATION: (272544)...(272643)
OTHER INFORMATION: n = A,T,C or G
FEATURE:
NAME/KEY: misc_feature
LOCATION: (279545)...(279644)
OTHER INFORMATION: n = A,T,C or G
FEATURE:
NAME/KEY: misc_feature
LOCATION: (300892)...(300991)
OTHER INFORMATION: n = A,T,C or G
FEATURE:
NAME/KEY: misc_feature

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; LOCATION: (327555)...(327654)
; OTHER INFORMATION: n = A,T,C or G
FEATURE:
NAME/KEY: misc_feature
LOCATION: (332849)...(332948)
OTHER INFORMATION: n = A,T,C or G
FEATURE:
NAME/KEY: misc_feature
LOCATION: (341698)...(341698)
OTHER INFORMATION: n = A,T,C or G
FEATURE:
NAME/KEY: misc_feature
LOCATION: (345190)...(345289)
OTHER INFORMATION: n = A,T,C or G
FEATURE:
NAME/KEY: misc_feature
LOCATION: (350504)...(350603)
OTHER INFORMATION: n = A,T,C or G
FEATURE:
NAME/KEY: misc_feature
LOCATION: (391524)...(391623)
OTHER INFORMATION: n = A,T,C or G
FEATURE:
NAME/KEY: misc_feature
LOCATION: (396625)...(396724)
OTHER INFORMATION: n = A,T,C or G
PCT-US03-32805-1

Query Match      73.3%; Score 37.4; DB 1; Length 398800;
Best Local Similarity 87.2%; Pred. No. 0.038; Indels 0; Gaps 0;
Matches 41; Conservative 0; Mismatches 6;

Cy          1 GAGGATGAAGCTGTGAAGAGAGAAGAGAGAGAGAGAGAGAGAAGA 47
            ||||| | | | | | | | | | | | | | | | | | | | | | |
Db          51856 GAGGAGGAAGATGAGGAAGATGAAGAGATGAGAGAGAGAGA 51902

RESULT 9
US-10-417-375A-1
Sequence 1, Application US/10417375A
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: Marc Malandro
TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
FILE REFERENCE: 529452001600
CURRENT APPLICATION NUMBER: US/10/417,375A
CURRENT FILING DATE: 2003-04-15
NUMBER OF SEQ ID NOS: 176
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 310122
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: (1)-(310122)
LOCATION: (1)-(310122)
OTHER INFORMATION: n = A,T,C or G
US-10-417-375A-1

Query Match      72.9%; Score 37.2; DB 6; Length 310122;
Best Local Similarity 84.0%; Pred. No. 0.042; Indels 0; Gaps 0;
Matches 42; Conservative 0; Mismatches 8;

Cy          1 GAGGATGAAGCTGTGAAGAGAGAAGAGAGAGAGAGAGAGAAGTGG 50
            ||||| | | | | | | | | | | | | | | | | | | | | |
Db          256497 GAAGAAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 256546

RESULT 10
US-10-767-701-24209
Sequence 24209, Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovallig, David K.
```

NUMBER OF SEQs: 1
 SEQ ID NO: 264
 LENGTH: 264
 TYPE: DNA
 ORGANISM: Sorghum bicolor
 FEATURE:
 OTHER INFORMATION: Clone ID: 3093345
 1
 72 24: Score 36.8; DB 6; Length 264; Gaps 0;
 244: Pred. Matches
 10-167-701-24205 Indels 0;
 0

OY

1 GAGGATCTTTTGGTGGAAGAATT
|||||
D8

166 GAGGACAAAGAACAGCGGAGGAACAATAA-
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```

US-0-767-471-1055 Application US-0-767-471-1055
US Sequence 10551055 MICHAEL E. AT AL.
GENERAL INFORMATION: MICHAEL E. AT AL.
APPLICANT INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
REUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: REUMATOID ARTHRITIS
FILE REFERENCE: CL001558 NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
CURRENT OF SEQ ID NOS: Windows Version 4.0
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 10555
LENGTH: 34304
TYPE: DNA
GENSM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature (34304)
LOCATION: (1)..(34304)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1
US-10-767-471-10555
72.2% Score 36.8; DB 6; Length 34304;
Pred. No. 0.046; 7; Indels 0; Gaps 0;
```

Query Match	Similarity	85.1%	0	Mismatch
Best Local	Conservative			
Matches	41			

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RESULT 12
US-10-417-375A-79 Application US/10417375A
Sequence 79, Application:
Description:

GENERAL INFORMATION
 INVENTOR: David W. Morris
 APPLICANT: Marc Malandro
 TITLE OF INVENTION: Novel
 Therapeutic Target
 NUMBER: 529452001600
 DATE: US/10/417,375A

```
FILE REFERENCE NUMBER: 2003-04-15  
CURRENT APPLICATION DATE: 176  
CURRENT FILING NOS: 176  
NUMBER OF SEQ ID NOS: 176  
PARTSEQ for Windows Version 4.0
```

SOFTWARE: FACT
SEQ ID NO 79
LENGTH: 54303
TYPE: DNA
MUS MUSCULUS

ORGANISM
MS-10-417-375A-79

[illegible]

RESULT 13
375A-63
US/10417375A

```

US-10-417-5-63. Applicant:
; Sequence Information: Morris
; General: David M. Malandro
; Applicant: Marc Malandro
; Title of Invention: Novel Therapeutic Targets in Cancer
; File Reference: 529432003.600
; Current Application Number: 2003-04-15
; Current Filing Date: 176
; Current SEQ ID NOS: 1
; Number of SEQ IDs for Windows Version 4.0
; Software: FastSeq
; SEQ ID NO: 219715
; Software: 63

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NAME/KEY:	"1" - (219,13)	DB 6:	length 219715;	0
LOCATION:	n = A, T, C or G			
OTHER INFORMATION:				
ns-10-417-375A-63	72.2%	Score 36.8;	indels 0;	Gaps 0
		No. 0.052;		
		7;		

Query Match	Similarity	85.4%	Prec.	Mismatches	
Best Local	41	Conservative	0		48
Matches					10709

[illegible]

RESULT 14
US-10-767-701-26619/c Application US/10767701

1-
; Sequence INFORMATION: David K.
; GENERAL INFORMATION: Kovalic, Yuhua
; APPLICANT: Zhou, Yongwei
; APPLICANT: Cao, Zhong
; APPLICANT: Nucleic Acid Molecules and Other Molecules Association
; APPLICANT: Tissues thereof For Plant Improvement

APPLICANT: plants and
TITLE OF INVENTION: B
TITLE OF INVENTION: US/10/767, 70
FILE REFERENCE: 38-21(53535)
PENDING APPLICATION NUMBER: 2004-01-29

```

CURRENT FILING DATE: 63128
CURRENT OF SEQ ID NOS:
NUMBER OF SEQ ID NOS: 26619
SEQ ID NO 26619
LENGTH: 650

```

```

; LENSE: DNA
; TYPE: Sorghum bicolor
; ORGANISM: Clone ID: 30976844
; FEATURE:
; OTHER INFORMATION:
; CC19
; DB 6: Length 650;

```

Query Match	Local Similarity	Conservative	Score	Pred. No.	0.063	7	Indels	0	0
US-10-767-701-2662	70.2%	85.1%	0	Mismatches	47				

[illegible]

94 GRC-
Db

US-10-767-701-13

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2004, 05:30:03 ; Search time 2156 Seconds

(without alignments)
706.387 Million cell updates/sec

Title: US-09-692-077D-1_COPY_880_930

Perfect score: 51
Sequence: 1 gagagatgaagctgaagaga.....aggagagagagagagatcgt 51

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: em_estba:*
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3: em_estin:*
4: em_estmu:*
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6: em_estro:*
7: em_estro:*
8: em_hcc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hcc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estin:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrt:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	1353	29	AY416856 Homo sapi
2	42	82.4	872	29	AL606560 Horse alp
3	41.6	81.6	430	28	AZ223727 RPT-23-6
4	41.6	81.6	469	9	AA943361 EST198860

C	5	41.6	81.6	517	10	BE097734
C	6	41.6	81.6	552	14	CF795982
C	7	41.6	81.6	604	9	AJ517718
C	8	41.6	81.6	713	28	AZ288043
C	9	40.6	79.6	640	12	BI067787
C	10	40.6	79.6	668	28	BH309086
C	11	40.6	79.6	723	13	BU121352
C	12	40.6	79.6	753	13	BE613618
C	13	40.6	79.6	797	28	AQ875889
C	14	40.6	79.6	826	28	BZ227940
C	15	40.6	79.6	873	13	BQ231724
C	16	40.6	79.6	1362	12	BM807097
C	17	40.4	79.2	453	10	BB852469
C	18	40.4	79.2	553	13	BX519271
C	19	40.4	79.2	786	28	AZ208950
C	20	40.4	79.2	799	28	BZ152227
C	21	40.4	79.2	834	28	BZ249816
C	22	40	78.4	152	28	BH108383
C	23	40	78.4	167	28	BH072396
C	24	40	78.4	256	14	CA315228
C	25	40	78.4	330	14	CF897938
C	26	40	78.4	331	9	AL135731
C	27	40	78.4	358	14	CD564037
C	28	40	78.4	365	13	BY054209
C	29	40	78.4	365	13	BY168255
C	30	40	78.4	373	14	CA538239
C	31	40	78.4	388	18	BY135560
C	32	40	78.4	413	28	BZ105773
C	33	40	78.4	444	13	BQ558077
C	34	40	78.4	446	10	BG076252
C	35	40	78.4	459	28	AZ554793
C	36	40	78.4	476	10	BB851808
C	37	40	78.4	512	14	CB272922
C	38	40	78.4	514	28	BZ089457
C	39	40	78.4	517	14	CB1716103
C	40	40	78.4	558	28	BZ159900
C	41	40	78.4	578	14	CA752540
C	42	40	78.4	586	9	AI451753
C	43	40	78.4	587	12	BG325179
C	44	40	78.4	594	14	CF796838
C	45	40	78.4	612	28	BZ149404

ALIGNMENTS

RESULT 1
LOCUS: AY416856
DEFINITION: Homo sapiens HCM6030 gene, VIRUAL TRANSCRIPT, partial sequence.
ACCESSION: AY416856
VERSION: AY416856.1 GI:39772816
KEYWORDS: GSS.
SOURCE: Homo sapiens (human)
ORGANISM: Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE: 1 (bases 1 to 1353)
AUTHORS: Clark A.G., Gianoweki, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civiello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J., Adams, M.D. and Cargill, M.
TITLE: Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL: Science 302 (5652), 1960-1963 (2003)
PUBMED: 14671302
REFERENCE: 2 (bases 1 to 1353)
AUTHORS: Clark, A.G., Gianoweki, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civiello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J., Adams, M.D. and Cargill, M.
TITLE: Direct Submission

JOURNAL

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

COMMENT

Location/Qualifiers

FEATURES

1..1353
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/locus_tag="HGM6030"

gene

ORIGIN

Query Match 100.0%; Score 51; DB 29; Length 1353;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GAGATGACCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 51

880 GAGATGACCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 930

RESULT 2

LOCUS

DEFINITION

ECOA2BAR 872 bp DNA linear GSS 14-SEP-2001
Horse alpha2 adrenergic receptor gene fragment probably subtype D.

genomic survey sequence.

VERSION

AL606560.1 GI:15591917
GSS: Alpha2 adrenergic receptor gene.

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

DEFINITION

FEATURES

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

Db

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GAGATGACCTGAAAGAGAGAGAGAGAGAGAGAGAGAGTGT 50

571

GAGATGACCTGAAAGAGAGAGAGAGAGAGAGAGAGAGTGT 620

RESULT 3

LOCUS

DEFINITION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1

(bases 1 to 430)

AUTHORS

Zhao, S., Nieman, W., Feldlyum, T., Malek, J., Shatsman, S.,
Akinret, B., Levine, M., Megann, S., Tsegaye, G., Geer, K., Krol, M., de
Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23

TITLE

JOURNAL

COMMENT

Other GSSs

RPCI-23-63A7.TV

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

7712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)

or from Resea ch Genetics (info@resgen.com). BAC end page:

http://www.tigr.org/cdb/bac_ends/mouse/bac_end_intro.html

Plate: 63 row: A column: 7

Seq primer: SP6

Class: BAC ends.

Location/Qualifiers

1..430

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-23-63A7"

/sex="Female"

/lab_host="DH10B"

/clone_1lb="RPCI-23"

/notes="Organ: Kidney/Brain; Vector: pBAC3.6; Site 1:

ECORI: Site 2: ECORI: Female C57BL/6J mouse kidney and/or

brain genomic DNA was isolated and partially digested

with a combination of ECORI and ECORI Methyase. Size

selected DNA was cloned into the pBAC3.6 vector at the

ECORI sites. The ligation products were transformed into

DH10B electrocompetent cells (BRL Life Technologies)."

ORIGIN

Query Match 81.6%; Score 41.6; DB 28; Length 430;
Best Local Similarity 91.7%; Pred. No. 43;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 GAGATGACCTGAAAGAGAGAGAGAGAGAGAGAGAGAGTGT 48

103 GAGATGACCTGAAAGAGAGAGAGAGAGAGAGAGAGAGTGT 56

AA943361 469 bp mRNA linear EST 16-JUN-1998

EST198860 Normalized rat brain, Bento Soares Rattus sp. cDNA clone

RBR164 3' end, mRNA sequence.

AA943361 1 GI:3103277

EST.

Rattus sp.

Rattus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 469)

Lee, N.H., Glodet, A., Chandra, I., Mason, T.M., Quackenbush, J.,

Kerlavage, A.R. and Adams, M.D.

Rat Genome Project: Generation of a Rat EST (REEST) Catalog & Rat

Gene Index

Unpublished (1998)

Contact: Lee, NH

The Institute for Genomic Research

7712, Medical Center Drive, Rockville, MD 20850, USA

Tel: (301)-838-3529

Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGA 47
|||||
180 GAAGAGGAAGATGAAGAGAGAGAGAGAGAGAGAGAGA 226

RESULT 10
BH309086/c 668 bp DNA linear GSS 03-DEC-2001
LOCUS CH230-4L16.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
DEFINITION CH230-4L16, genomic survey sequence.
ACCESSION BH309086
VERSION BH309086.1 GI:17234555
KEYWORDS GSS.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 668)
Shvartbeyn,A., Gebregorgis,E., Overton,L., Russell,D., Chen,D.,
Riggs,P., de Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 EcORI segment
Unpublished (1999)
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdj@jngemail.chc.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/orfing/information.htm). BAC end
page: http://www.tigr.org/cdb/bac_end/rat/bac_end_intro.html
1 place: 4 row: 1 column: 16
Seq primer: 77
Class: BAC ends.
FEATURES
Location/Qualifiers
1..668
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SAHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-4L16"
/sex="Female"
/cell_type="Brain"
/clone_1lb="CHORI-230 Segment 1"
/note="Vector: PTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
CHORI-230 Rat (BN/SAHsd/MCW) BAC library produced by
Pieter de Jong"

ORIGIN
Query Match 79.6%; Score 40.6; DB 28; Length 668;
Best Local Similarity 91.5%; Pred. No. 71;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGA 47
|||||
164 GAGAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 118

RESULT 11
BU121352 723 bp mRNA linear EST 25-NOV-2002
LOCUS BU121352
DEFINITION 603146064F1 CSEQCHL17 Gallus gallus cDNA clone CHEST145016 5', mRNA
sequence.
ACCESSION BU121352
VERSION BU121352.1 GI:25331126

KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 723)
Bardman,P.E., Sanz-Bzquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
JOURNAL MEDLINE 2235534
PUBMED 12445392
CONTACT Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES
source
1..723
Location/Qualifiers
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="CHEST145016"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_1lb="CSEQCHL17"
/note="Organ: kidney + adrenal; Vector: pBluescript II
KS(+); Site 1: EcoRI; Site 2: NotI. Modification of
pBluescript II KS(+) [Stratagene] vector to accommodate
cDNA produced with the T-primed protocol (Construction of
uni-directionally cloned cDNA libraries from messenger RNA
for improved 3' end DNA sequencing by Glenn Fu, et al.
U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with
NotI and EcoRI. Ligate in double stranded adaptor
containing BglI and BamHI sites
[5'ggcgccgctgcagcccgatccgcaagc]
[5'aattcttttcgagatccgggctcgcaagc]"

ORIGIN
Query Match 79.6%; Score 40.6; DB 13; Length 723;
Best Local Similarity 91.5%; Pred. No. 72;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGA 47
|||||
648 GAAGAGGAAGATGAAGAGAGAGAGAGAGAGAGAGAGA 694

RESULT 12
BE613618 753 bp mRNA linear EST 20-OCT-2000
LOCUS BE613618
DEFINITION 601504406F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:396193 5',
mRNA sequence.
ACCESSION BE613618
VERSION BE613618.1 GI:9895215
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 753)
NIH-MGC http://mhc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
CONTACT Robert Strausberg, Ph.D.
Email: cgepps-remail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1AM9714 row: 1 column: 02
 High quality sequence stop: 711.

FEATURES

source

Location/Qualifiers
 1..753

/organism="Homo sapiens"
 /mol_type="mrna"
 /db_xref="taxon:9606"
 /clone="IMAGE:3906193"
 /isue_type="leiomysarcoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="NH_MGC_71"
 /note="Organ: uterus; Vector: PCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 2.1 kb."

ORIGIN

Query Match
 Best Local Similarity 79.6%; Score 40.6; DB 10; Length 753;
 Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGA 47
 27 GAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 73

RESULT 13
 LOCUS A0875889 797 bp DNA linear GSS 08-NOV-1999
 DEFINITION VJ30F6 mtn-3xHA/lacZ insertion library, strain Y2278 Saccharomyces
 cerevisiae genomic 5', genomic survey sequence.
 VERSION A0875889
 KEYWORDS GSS.
 SOURCE Saccharomyces cerevisiae (baker's yeast)
 ORGANISM Saccharomyces cerevisiae

REFERENCE
 AUTHORS 1 (bases 1 to 797)
 deatages, S.A., Cheung, K.-H., Sheehan, A., Symonatsis, D., Jansen, R.,
 Hager, K., Miller, P., Roeder, G.S., and Snyder, M.
 Large-Scale Analysis of the Yeast Genome by Transposon Tagging and
 Gene Disruption
 Unpublished (1999)

TITLE

JOURNAL
 COMMENT Contact: Kumar A
 Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
 Yale University
 P.O. Box 208103, New Haven, CT 06520-8103, USA
 Tel: 203 432 9949
 Fax: 203 432 6161
 Email: amuj.kumar@yale.edu
 te of mtn-3xHA/lacZ insertion.
 Seg primer: GGCCTTCCTTCCTTGGAGACTAC
 Class: transposon-tagged

FEATURES

source

Location/Qualifiers
 1..797

/organism="Saccharomyces cerevisiae"
 /mol_type="genomic DNA"
 /strain="Y2278 - S288C background, cir(0) rho(0)"
 /db_xref="taxon:4932"
 /lab_host="E. coli"
 /clone_id="mtn-3xHA/lacZ insertion library, strain Y2278"
 /note="Vector: pHS6-Sal; A yeast genomic DNA library
 without 2 micron or mitochondrial DNA was prepared in
 pHS6-Sal; genomic DNA was size-fractionated (DNA of
 roughly 2-3 kb in length) prior to cloning. This library

ORIGIN

Query Match
 Best Local Similarity 79.6%; Score 40.6; DB 28; Length 797;
 Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGA 47
 260 GAGGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 306

RESULT 14
 LOCUS B2227940/c 826 bp DNA linear GSS 12-OCT-2002
 DEFINITION CH230-400D22.TU CHORI-230 Segment 2 Rattus norvegicus genomic clone
 CH230-400D22, genomic survey sequence.
 VERSION B2227940
 KEYWORDS B2227940.1 GI:23886481
 GSS.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus

REFERENCE
 AUTHORS 1 (bases 1 to 826)
 Zhao, S., Shetty, J., Shatman, S., Tesagye, G., Geer, K.,
 Shvartsbeyn, A., Gebregorgis, E., Overton, L., Russell, D., Chen, D.,
 Riggs, F., de Jong, P. and Fraser, C.M.
 Rat BAC End Sequences from Library CHORI-230 Mbol segment
 Unpublished (1999)

TITLE

JOURNAL
 COMMENT Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230
 (http://www.chori.org/bacpac/rat230.htm). For BAC library
 availability, please contact Pieter de Jong (pdejong@mail.choi.org).
 Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/or ering_information.html). BAC end
 page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
 Plate: 400 row: D column: 22
 Seg primer: SP6
 Class: BAC ends.

FEATURES

source

Location/Qualifiers
 1..826

/organism="Rattus norvegicus"
 /mol_type="genomic DNA"
 /strain="BN/SnHsd/MCW"
 /db_xref="taxon:10116"
 /clone="CH230-400D22"
 /sex="Female"
 /cell_type="Brain"
 /clone_id="CHORI-230 Segment 2"
 /note="Vector: pTARBA1.3; Site 1: Mbol; Site 2: Mbol;
 CHORI-230 Rat (BN/SnHsd/MCW) BAC library produced by
 Pieter de Jong"

ORIGIN

Query Match
 Best Local Similarity 79.6%; Score 40.6; DB 28; Length 826;
 Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGA 47
 794 GAGGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 748

was subsequently mutagenized with a mtn-3xHA/lacZ
 minitransposon containing lacZ, URA3, and tet resistance.

RESULT 15
 BQ231724 873 bp mRNA linear EST 02-MAY-2002
 LOCUS AGENCOURT_7560029 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6055864
 DEFINITION 5', mRNA sequence.
 ACCESSION BQ231724
 VERSION BQ231724.1 GI:20413124
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 873)
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTP
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLNL13316 row: m column: 17
 High quality sequence stop: 703.
 Location/Qualifiers

FEATURES

source
 1..873
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6055864"
 /issue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="NIH MGC 72"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2 kb. Library constructed by Life
 Technologies."

ORIGIN

Query Match 79.6%; Score 40.6; DB 13; Length 873;
 Best Local Similarity 91.5%; Pred. No. 74;
 Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 GAGATGAGCTGAGAGGAGAGAGAGAGAGAGAGAGAGA 47
 |||||
 Db 103 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 149
 |||||

Search completed: March 2, 2004, 08:34:35
 Job time: 2156 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2004, 04:47:22 ; Search time 864.5 Seconds

(without alignment)
2556.963 Million cell updates/sec

Title: US-09-692-077d-2_COPY_880_930

Perfect score: 1 gagagtagagctgaagagga.....aggaagagctggaacccag 51

Sequence: 51 gagagtagagctgaagagga.....aggaagagctggaacccag 51

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank:

1: gb_ba:*

2: gb_hg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sec:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: gb_ba:*

16: gb_fun:*

17: gb_hum:*

18: gb_in:*

19: gb_mu:*

20: gb_om:*

21: gb_or:*

22: gb_ov:*

23: gb_pat:*

24: gb_ph:*

25: gb_pl:*

26: gb_ro:*

27: gb_sec:*

28: gb_sy:*

29: gb_un:*

30: gb_vl:*

31: gb_ba:*

32: gb_hg:*

33: gb_in:*

34: gb_om:*

35: gb_ov:*

36: gb_pat:*

37: gb_ph:*

38: gb_pl:*

39: gb_ro:*

40: gb_sec:*

41: gb_sy:*

42: gb_un:*

43: gb_vl:*

44: gb_ba:*

45: gb_fun:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	51	100.0	246	10	S6731752	S67319 alpha 2-adr
2	51	100.0	188	10	S67316	S67316 alpha 2-adr
3	51	100.0	1344	6	AX350490	AX350490 Sequence
4	51	100.0	1344	9	AF316895	AF316895 Homo sapi
5	51	100.0	22842	9	AC092603	AC092603 Homo sapi
6	46.2	90.6	1168	4	PVT25176	PVT25176 Phoca vit
7	43	84.3	1180	4	LPA505821	LPA505821 Lama paco
8	43	84.3	1180	4	LPA505821	LPA505821 Lama paco
9	41.8	82.0	6904	6	AX344976	AX344976 Sequence
10	41.8	82.0	6904	6	AX344976	AX344976 Sequence
11	41.6	81.6	885	9	HUMA2C2	HUMA2C2 Human alpha
12	41.6	81.6	1030	9	HSB325747	HSB325747 Homo sapi
13	41.6	81.6	1353	6	AX350489	AX350489 Sequence
14	41.6	81.6	2072	6	AR270618	AR270618 Sequence
15	41.6	81.6	2072	6	HUMADRA2RA	HUMADRA2RA Human alpha
16	41.6	81.6	3374	6	AX548756	AX548756 Sequence
17	41.6	81.6	9944	9	AF005900	AF005900 Homo sapi
18	41.4	81.2	1180	9	NC0251186	NC0251186 Hyleicebu
19	41.4	81.2	1218	10	TPA427262	TPA427262 Thymomys
20	39.8	78.0	1179	10	TPA427262	TPA427262 Thymomys
21	38.8	76.1	1347	10	AF332049	AF332049 Mus muscu
22	38.8	76.1	1347	10	AF332050	AF332050 Mus muscu
23	38.8	76.1	1650	10	MUSADRENH	MUSADRENH Mus musculi
24	38.8	76.1	2319	10	RATADBR	RATADBR Rattus no
25	38.8	76.1	6268	10	AF366899	AF366899 Rattus no
26	38.8	76.1	9377	10	MUSADRECA	MUSADRECA Mus musculi
27	38.8	76.1	83802	10	AL731836	AL731836 Mouse DNA
28	38.8	76.1	124474	2	AC126878	AC126878 Rattus no
29	38.8	76.1	261258	2	AC091365	AC091365 Rattus no
30	38.8	76.1	276543	2	AC112830	AC112830 Rattus no
31	38.4	75.3	1639	10	RNA2BARA	RNA2BARA Rattus no
32	38.2	74.9	1173	4	EAT419810	EAT419810 Emballionu
33	38.2	74.9	1180	10	CRO271336	CRO271336 Cavia por
34	38.2	74.9	1188	4	RTU419814	RTU419814 Rhogesa
35	38.2	74.9	1198	4	ECAR2B	ECAR2B Equus cabal
36	38.2	74.9	1356	4	AY150333	AY150333 Tupala de
37	37.2	72.9	194614	2	AC113944	AC113944 Mus muscu
38	37.2	72.5	301817	2	AC095571	AC095571 Rattus no
39	36.6	71.8	1180	4	HAM251178	HAM251178 Hippopota
40	36.6	71.8	1185	10	EDO427270	EDO427270 Erethizon
41	36.6	71.8	1185	10	ASPA427259	ASPA427259 Anomaluru
42	36.6	71.8	1203	4	TE315939	TE315939 Tapirus t
43	36.4	71.4	1547	10	AY341886	AY341886 Rattus no
44	36.4	71.4	143350	2	AC121509	AC121509 Mus muscu
45	36.4	71.4	241678	2	AC121484	AC121484 Rattus no

ALIGNMENTS

RESULT 1
S6731752
LOCUS S6731752 246 bp mRNA ROD 26-FEB-1994
DEFINITION alpha 2-adrenergic receptor [rats, Sprague-Dawley, 5 month old
pancreas, mRNA Partial, 246 nt, segment 2 of 2].
ACCESSION S67319
VERSION S67319.1 GI:456951
KEYWORDS
SEGMENT 2 of 2
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (baaes 1 to 246)


```

CDS
    1..1344
        /gene="ADRA2B"
        /note="G-protein coupled receptor"
        /codon_start=1
        /product="alpha 2B adrenergic receptor"
        /protein_id="AAK01635.1"
        /db_xref="GI:12698670"
        /translation="MDHDDPYSVQATAIAAATPELITPTIGNALVLVAITSRLS
APQVLFLVSLAADILVALTLIIPSTLANELLGYFRTTVEVLAIDLVCSTIVH
LCALISLDRIYAVSRDALEYNRSRTPRRKICILLTWLNAVISLPPLIKGGQGPDR
RPOKLQDAWYVIILASISGSFFPCLILVLYLRILYLAKNSNRGPRACKPGQGES
KOPPDHGALASAKLPAIASVASAREVNGHSKTGESEETPEDTRALPSMAABE
LPNQGOGKEGVCSGEDBAEEBESECEBPQAVPVSPASCPPIQQPGSGRYLAR
TLRGDGLRGVGAIGCGMWRRAQLTEKRFTLVIVICVPILCCPPFPFSYLG
ICPHCKVPHELPFPPFWIGYCNSLNVEYITTFINODFRARFRILCPWTQTAM"
            891 892
        /gene="ADRA2B"
        /note="compared to wild type sequence presented in GenBank
Accession Number AF005900; polymorphic sequence lacks
three glu residues at this location"
        /frequency="Caucasians 0.31; African-Americans 0.12"
        /replace="gaagaggag"

ORIGIN
Query Match      100.0%; Score 51; DB 9; Length 1344;
Beet Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;
Matches 51; Conservative 0; Perfect 0;

Oy      1 GAGGTGTAAGCTGAAGACGAGAGGAGGAGAAGAGTGTTGAACCCGAG 51
       |||
Db      880 GAGATGAAGCTGAAGACGAGAGGAGAGAGAGAGAGAGTGTGAACCCGAG 930

RESULT 5
LOCUS      AC092603              22842 bp    DNA         linear     PRI 01-MAR-2002
DEFINITION Homo sapiens BAC clone RP11-139J6 from 2, complete sequence.
VERSION    AC092603 AC073396
KEYWORDS   HTG.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 22842)
AUTHORS   Sulston,J.E. and Waterston,R.
TITLE     Toward a complete human genome sequence
JOURNAL   Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE   99063792
PUBMED    9847074
REFERENCE  2 (bases 1 to 22842)
AUTHORS   Matcinka,S., Abbott,A., Hawkins,M., Elliott,G. and Doeber,A.
TITLE     The sequence of Homo sapiens BAC clone RP11-139J6
JOURNAL   Unpublished (2001)
REFERENCE  3 (bases 1 to 22842)
AUTHORS   Waterston,R.H.
TITLE     Direct Submision
JOURNAL   Submitted (19-JUL-2001) Genome Sequencing Center, Washington
UNIVERSITY School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE  4 (bases 1 to 22842)
AUTHORS   Waterston,R.H.
TITLE     Direct Submission
JOURNAL   Submitted (20-OCT-2001) Genome Sequencing Center, Washington
UNIVERSITY School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE  5 (bases 1 to 22842)
AUTHORS   Waterston,R.H.
TITLE     Direct Submission
JOURNAL   Submitted (23-OCT-2001) Genome Sequencing Center, Washington
UNIVERSITY School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE  6 (bases 1 to 22842)

```

AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT On Oct 20, 2001 this sequence version replaced gi:14916188.

Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc>
 Contact: sapiens@watson.wustl.edu
 ----- Summary Statistics -----
 Center project name: H_NH013906
 Drafting Center: MIBR

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION: The RPcrl-11 human BAC library was made from the blood of one male donor, as described by Otagawa, K., Moon, P. Y., Zhao, B., Frengen, E. Tanono, M., Caranese, J. J. and de Jong, P. J. (1998). An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-401C13, 2000 bp overlap;
the clone sequenced to the right is RP11-574O17, 2000 bp overlap.
Actual end of this clone is at base position 48999 of RP11-574O17.

Polymorphisms have been identified between AC013272 and AC092603.

The sequence of AC073396 has been incorporated into AC092603.

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/chromosome="2"
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1424..1449
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1495..1665
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1669..1966
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2812..2918
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Best Local Similarity 100.0%; Pred.No. 6.3e-05;
Matches          51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
LOCUS              PV1251176                1168 bp    DNA             linear    MAM 01-JUN-2001
DEFINITION         Phoca vitulina partial aar2b gene for alpha adrenergic receptor 2B.
ACCESSION           AJ251176
VERSION             AJ251176.1 GI:11322419
KEYWORDS            aar2b gene; alpha adrenergic receptor 2B.
SOURCE              Phoca vitulina (harbor seal)
ORGANISM            Mammalia; Euteleostomi;
AUTHORS             Madgen O., Scally, M., Donady, C.J., Kao, D.-J., DeBry, R.W., Adkins, R.,
                    Amrine, H.M., Stanhope, W.J., de Jong, W.W. and Springer, M.S.
TITLE               Parallel adaptive radiations in two major clades of placental
                    mammals
JOURNAL             Nature 409 (6820), 610-614 (2001)
MEDLINE             PUBMED 11214318
REFERENCE           2 (bases 1 to 1168)
AUTHORS             Madgen, O.
TITLE               Direct Submission
JOURNAL             Submitted (18-NOV-1999) Madgen O., Department of Biochemistry,
                    University of Nijmegen, P.O. box 9101, 6500 HB Nijmegen,
                    NETHERLANDS

FEATURES
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Db 833 GAGGAGGAAGCTGAAAGAGGAGAGGAGAGGAGGAAGAGTGTGAGCCTCAG 893

RESULT 7
LPA505821 1180 bp DNA linear MAM 12-DEC-2002

LOCUS
LPA505821

DEFINITION
Lama pacos partial adra2b gene for alpha 2B adrenergic receptor.

ACCESSION
AJ505821

VERSION
AJ505821.1 GI:22324219

KEYWORDS
adra2b gene; alpha 2B adrenergic receptor.

SOURCE
Lama pacos (alpaca)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.

REFERENCE
1
Madsen, O., Willmsen, D., Ursing, B.M., Arnason, U. and de Jong, W.M. Molecular evolution of the mammalian alpha 2B adrenergic receptor Mol. Biol. Evol. 19 (12), 2150-2160 (2002)

REFERENCE
2
Madsen, O., Willmsen, D., Ursing, B.M., Arnason, U. and de Jong, W.M. Molecular evolution of the alpha 2B adrenergic receptor Unpublished (bases 1 to 1180)

REFERENCE
3
Madsen, O. Direct Submission Submitted (14-AUG-2002) Madsen O., 161 Biochemistry NMI, University of Nijmegen, PO BOX 9101, 6500HB Nijmegen, NETHERLANDS

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ORIGIN
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Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAGATGAAGCTGAAAGAGGAGGAGGAGGAGGAAGAGTGTGAACCCAG 51
Db 845 GAGAGGAGGCGCTGCAGAGGAGGAGGAGGAGGAAGAGTGTGAGCCTCAG 895			

RESULT 8
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LOCUS
LPA315941
DEFINITION
Lama pacos partial adra2b gene for alpha 2B adrenergic receptor.
ACCESSION
AJ315941
VERSION
AJ315941.1 GI:21212927
KEYWORDS
adra2b gene; alpha 2B adrenergic receptor.
Lama pacos (alpaca)

ORGANISM	Lama pacos
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
AUTHORS	Murphy,W.J., Elzirik,E., O'Brien,S.J., Madsen,O., Scally,M., Donady,C.J., Teeling,E., Ryder,O.A., Stanhope,M.J., de Jong,W.W. and Springer,M.S.
TITLE	Resolution of the early placental mammal radiation using Bayesian phylogenetics
JOURNAL	Science 294 (5550), 2348-2351 (2001)
MEDLINE	21608557
PUBMED	11743200
REFERENCE	2 (bases 1 to 1197)
AUTHORS	Madsen,O.
TITLE	Direct Submission
JOURNAL	Submitted (14-AUG-2001) Madsen O., 161 Biochemistry NWI, University of Nijmegen, P.O.Box 9101, 6500 HB Nijmegen, NETHERLANDS
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Best Local Similarity	50.2%; Pred. No. 0.014;
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AX344976	6904 bp DNA linear PAT 01-FEB-2002
LOCUS	AX344976
DEFINITION	Sequence 47 from Patent WO200928.
ACCESSION	AX344976
VERSION	AX344976.1 GI:18492862
KEYWORDS	.
SOURCE	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1
AUTHORS	Olek,A., Piepenbrock,C. and Berlin,K.
TITLE	Diagnosis of diseases associated with the immune system
JOURNAL	Patent: WO 0200928-A 47 03-JUN-2002;
FEATURES	Bipogenomics AG (DB) Location/Qualifiers
source	1..6904 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Chemically treated genomic DNA (Homo sapiens)"
ORIGIN	

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DB 187 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAAAGTGTGAACCCCGAG 140

RESULT 13
AX350489
LOCUS AX350489 1353 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 1 from Patent WO0179561.
ACCESSION AX350489
VERSION AX350489.1 GI:18616091
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Liggett, S.B. and Small, K.M.
TITLE Alpha-2 adrenergic receptor polymorphisms
JOURNAL Patent: WO 0179561-A 1 25-OCT-2001;
Liggett, Stephen B. (US) ; Small, Kersten M. (US)
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source 1.1353
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Best Local Similarity 91.7%; Pred. No. 0.036;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GATGAAGCTGAAGAGAGAGAGAGAGAGAAAGTGTGAACCCCGAG 51
DB 892 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAAAGTGTGAACCCCGAG 939

RESULT 14
AR270618
LOCUS AR270618 2072 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 1181 from patent US 6500938.
ACCESSION AR270618
VERSION AR270618.1 GI:29701852
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2072)
AUTHORS Au-Young, J. and Seilhamer, J.J.
TITLE Composition for the detection of signaling pathway gene expression
JOURNAL Patent: US 6500938-A 1181 31-DEC-2002;
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source 1.2072
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Best Local Similarity 91.7%; Pred. No. 0.035;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GATGAAGCTGAAGAGAGAGAGAGAGAGAAAGTGTGAACCCCGAG 51
DB 1304 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAAAGTGTGAACCCCGAG 1351

RESULT 15
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LOCUS HUMADRA2RA 2072 bp DNA linear PRI 30-OCT-1994
DEFINITION Human alpha-2-adrenergic receptor (alpha-2 c2) gene, complete cds.
ACCESSION M34041
VERSION M34041.1 GI:178197
KEYWORDS alpha-2-adrenergic receptor; plasma membrane protein;

SOURCE receptor-coupled G protein.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2072)
AUTHORS Lomasney, J.W., Lorenz, W., Allen, L.F., King, K., Regan, J.W.,
Yang-Feng, T.L., Caron, M.G. and Lefkowitz, R.J.
TITLE Expansion of the alpha 2-adrenergic receptor family: cloning and
characterization of a human alpha 2-adrenergic receptor subtype,
the gene for which is located on chromosome 2
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (13), 5094-5098 (1990)
MEDLINE 90311349
PUBMED 2164221
COMMENT Original source text: Human placenta DNA, clone alpha-2 C2.
Draft entry and computer-readable sequence for [1] kindly submitted
by J.W.Lomasney, 03-MAY-1990, for release after publication.

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Location/Qualifiers
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name 'ADRA2RL1'"
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ORIGIN Chromosome 2.
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DB 1304 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAAAGTGTGAACCCCGAG 1351

Search completed: March 2, 2004, 06:08:06
Job time : 865.5 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: March 2, 2004, 04:46:17 ; Search time 267.5 Seconds
(without alignment)

809.937 Million cell updates/sec

Title: US-09-692-077d-2_COPY_880_930

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Sequence: 1

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues
Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	51	100.0	828	9	ADB59041 Toxicity-
2	51	100.0	1344	4	AA199906 Human aip
3	47.8	93.7	1344	5	AA004761 Aa044388 Human aip
4	47.8	93.7	1344	6	AA044388 Human aip
5	41.8	82.0	6904	6	AB132074 Human aip
6	41.8	82.0	6904	6	AA028364 Human che
7	41.6	81.6	1353	4	AA199905 Human aip
8	41.6	81.6	1353	5	AA044762 Human aip
9	41.6	81.6	1353	6	AA044389 Human aip
10	41.6	81.6	2064	2	AA014151 Aa044388 Human aip
11	41.6	81.6	2064	2	AA159499 Human aip
12	41.6	81.6	2072	7	ACA56583 Human aip
13	41.6	81.6	3274	4	AB242624 Human aip
14	36.6	71.8	593	4	AA069332 3' end of
15	36	70.6	2367	7	ABR20256 Aspergill
16	36	70.6	2367	7	ABR20854 Aspergill
17	36	70.6	4238	7	ABR17846 Aspergill
18	36	70.6	4367	7	ABR19660 Aspergill
19	35	66.6	1429	3	AA054146 Arabidops
20	35	66.6	1820	3	AA088817 Human sur
21	34.4	67.5	392	6	ABN76609 Human ORF
22	34.4	67.5	5000	2	AAV25477 Rat snlph
23	34.4	67.5	5000	7	ABT1889 Toxicity

C	24	34.4	67.5	6628	9	ADB58175	Adbs8115	Toxicity-
	25	34.4	67.5	6628	9	ADB52677	Primary r	
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	27	33.8	66.3	291	5	AA68926	DNA encod	
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	35	33.4	65.5	2981	9	ADB85264	Mouse RNA	
	36	33.4	65.5	101786	3	AA022293	BAC cont	
	37	33.2	65.1	193	4	AA125502	Probe #15	
	38	33.2	65.1	193	4	ABA71654	Human toe	
	39	33.2	65.1	193	4	AA151949	Probe #20	
	40	33.2	65.1	193	4	ABA37774	Probe #16	
	41	33.2	65.1	193	4	AAK46037	Human bon	
	42	33.2	65.1	193	4	AAK19996	Human bra	
	43	33.2	65.1	193	4	AB45742	Human liv	
	44	33.2	65.1	193	6	AB820332	Human gen	
C	45	33.2	65.1	324	2	AAV89689	EST clone	

ALIGNMENTS

RESULT 1
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ID ADB59041 standard; DNA; 828 BP.
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AC ADB59041;
XX
DT 04-DEC-2003 (first entry)
XX
DE Toxicity-related gene, SEQ ID 4067.
XX
KW Toxic, toxin; gene expression profile; hepatotoxicity; liver;
XX drug screening; toxicity assay; de.
XX
OS Unidentified.
XX
PN WO2003064624-A2.
XX
PD 07-AUG-2003.
XX
PF 31-JAN-2003; 2003WO-US003194.
XX
PR 31-JAN-2002; 2002US-0006087.
XX 15-MAR-2002; 2002US-036405P.
XX 15-MAR-2002; 2002US-0364055P.
XX 30-DEC-2002; 2002US-0436643P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;
XX WPI; 2003-689530/65.
XX
PT Predicting a toxic effect of a compound, useful in identifying toxicity
XX markers in liver tissues or cells for drug screening and toxicity assays;
XX PT comprises preparing gene expression profile of tissue or cells exposed to
XX the compound.
XX
PS Claim 1; SEQ ID NO 4067; 1156bp; English.
XX
CC The present invention relates to a method for predicting a toxic effect
CC of a compound. The method comprises preparing a gene expression profile
CC of a tissue or cell sample exposed to the compound, and comparing the
CC gene expression profile to a database comprising SEQ ID 1-4925, where
CC differential expression of the gene indicates at least one toxic effect.
CC The method is useful for predicting at least one toxic effect of a
CC compound, predicting hepatotoxicity or the progression of a toxic effect

DR	WP1; 2001-300318/731.
DR	P-PSDB; AAE00989.
PT	New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular loop of the polypeptide, for treating vascular contraction of coronary arteries.
PS	Claim 3; Page 24-26; 37pp; English.
CC	The present sequence is a gene encoding human alpha2B-adrenoceptor (alpha2B-AR) variant protein. Alpha2B-AR has a glutamic acid repeat element (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino acids (amino acids 294-311), located in the third intracellular loop of the receptor polypeptide. The variant is obtained by deletion of three glutamates from the Glu repeat (amino acids 307-309). Alpha2B-AR gene is located on chromosome 2. Alpha2-AR mediate many of the physiological effects of the catecholamines, norepinephrine and epinephrine. An antagonist of alpha2B-adrenoceptor is useful for treating a mammal suffering from vascular contraction of coronary arteries and a disease involving vascular contraction of coronary arteries which is clinically expressed as coronary heart disease (CHD), unstable chronic angina pectoris which is clinically expressed as Prinzmetal's variant form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in gene therapy
SQ	Sequence 1344 BP; 219 A; 459 C; 400 G; 266 T; 0 U; 0 Other;
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Query Match	93.7%; Score 47.8; DB 5; Length 1344;
Best Local Similarity	96.1%; Pred. No. 0.00057;
Matches	49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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ID	AAD44388 standard; DNA; 1344 BP.
XX	
XX	AAD44388;
DT	13-DEC-2002 (first entry)
XX	
DE	Human alpha-2B-adrenoceptor variant DNA.
KW	Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;
KM	hypertension; hypotensive; variant; gene; da.
OS	Homo sapiens.
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	CDS 1..1344
FT	/product= "Human alpha-2B-adrenoceptor variant protein"
PN	WO200266617-A1.
XX	
PD	29-AUG-2002.
XX	
PF	13-FEB-2002; 2002MO-FI000113.
XX	
PR	20-FEB-2001; 2001FI-00000323.
XX	
PA	(JURI-) JURILAB LTD OY.
PI	Salonen J;
XX	
WI	WP1; 2002-667063/71.
DR	P-PSDB; AAE26633.
XX	

PT	Detecting a risk of hypertension and targeting treatment in a subject by
PT	determining the pattern of alleles encoding a variant alpha-2-
PT	adrenoceptor.
XX	
PS	Disclosure; Page 24-26; 35pp; English.
XX	
CC	The invention relates to a method for detecting a risk of hypertension by
CC	determining the pattern of alleles encoding a variant alpha-2B-
CC	adrenoceptor (AR) protein. The methods and compositions of the invention
CC	are useful for detecting risks and targeting treatment for hypertension.
CC	The kit is also useful for selecting for clinical drug trials testing the
CC	antihypertensive effect of compounds. The present sequence is human alpha-
CC	-2B-adrenoceptor variant DNA
XX	
SQ	Sequence 1344 BP; 219 A; 459 C; 400 G; 266 T; 0 U; 0 Other;
OY	
Db	
1	GAGCATGATGACTGAAGAGGAGGAGGAGGAGAAGAGTGTCGAACCCAG 51
880	GAGGATGAACTGTGAAGAGGAGAAGAGGAGGAGGAGGAGTGTGAACCCAG 930
RESULT 5	
ABLJ32074	
ID	ABLJ32074 standard; DNA; 6904 BP.
AC	ABLJ32074;
XX	
DT	26-MAR-2002 (first entry)
XX	
DE	Human immune system associated gene SEQ ID NO: 47.
XX	
KW	Human; immune system disease; cytosine methylation; antiasthmatic;
KW	antiarteriosclerotic; antihaemic; cyrostatic; noctropic;
KW	neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW	antirheumatic; antiarthritic; antidiabetic; antipsoiatric;
KW	antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW	acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW	neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
KW	ds.
XX	
OS	Homo sapiens.
XX	
PN	MO200200928-A2.
PD	
XX	
XX	03-JAN-2002.
XX	
XX	02-JUL-2001; 2001WO-BP007537.
XX	
PF	30-JUN-2000; 2000DE-01032529.
PR	01-SEP-2000; 2000DE-01043826.
XX	
PA	(EPig-) EPIGENOMICS AG.
XX	
P1	Olek A, Piepenbrock C, Berlin K;
DR	WPI; 2002-130909/17.
XX	
PT	Nucleic acid comprising fragment of chemically modified gene, useful for
PT	diagnosis and treatment of diseases associated with abnormal cytosine
PT	methylation.
XX	
PS	Claim 1; SEQ ID NO 47; 32pp + Sequence Listing; German.
XX	
CC	The present invention provides a number of human immune system associated
CC	genes which are modified by the methylation of cytosines. The sequences
CC	can be used in the diagnosis and treatment of immune system disorders,
CC	including eye diseases such as retinopathy, neovascular glaucoma and
CC	mucular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC	leukemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,

PF 30-JAN-1998; 98US-00016434.
XX
PR 30-JAN-1998; 98US-00016434.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
XX
PI Au-Young J, Selhammer JJ;
XX
DR WPI; 2003-352189/33.
XX
XX
PT Combination of polynucleotide probes, useful as array elements in a
PT microarray for monitoring the expression of a number of target
PT polynucleotides.

Claim 1; SEQ ID NO 1181; 65bp; English.

CC The invention relates to a combination which, comprises a number of
CC polynucleotide probes comprising a sequence selected from one of the 1496
CC sequences mentioned in the specification. The combination is useful as a
CC array element in a microarray for monitoring the expression of a number
CC of target polynucleotides. The microarray is particularly useful in the
CC diagnosis and treatment of cancer and immunopathology and neuropathology
CC The microarray is useful in diagnostics and treatment regimens, drug
CC discovery and development, toxicological and carcinogenicity studies,
CC forensics and pharmacogenomics. The microarray is also useful for
CC monitoring progression of diseases and for developing sophisticated
CC profiles for the effects of currently available therapeutic drugs. The
CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC and genomic fragments and in research and diagnostic applications. The
CC array can detect changes in expression in a large number of genes coding
CC for different signaling pathway populations which can be used to diagnose
CC various diseases including cancer e.g., adenocarcinoma and leukemia,
CC immunopathies e.g., AIDS and asthma, neuropathies e.g., Alzheimer's disease,
CC and Parkinson's disease. The present sequence represents a polynucleotide
CC probe of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=06500938&B1
XQ
XQ Sequence 2072 BP; 316 A; 705 C; 660 G; 391 T; 0 U; 0 Other;

	Query Match	81.6%	Score 41.6;	DB 7,	Length 2072;
	Best Local Similarity	91.7%	Pred. No. 0.02;		
Matches	44;	Conservative	0;	Mismatches	4; Indels 0; Gaps 0.
OY	4	GATGAAGCTGAAAGAGAGAGAAGAGAGAGTGTGAACCCCGA	51		
b	1304	GAACAAGAGCAAGAGAGAGAGAAGAGAGTGTTGAACCCCAG	1351		

RESULT 13
ABZ42624
ID ABZ42624 standard; DNA; 3274 BP

AC ABZ42624 ;

DT 04-MAR-2003 (first entry)

Human alpha 2b-adrenoceptor nucleotide SEQ ID NO:41

KM G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KM G protein-coupled receptor modulator; antibody; immune-related disease;
KM growth-related disease; cell regeneration-related disease; AIDS; cancer;
KM immunological-related cell proliferative disease; autoimmune disease;
KM Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy
KM osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KM graft versus host disease; Parkinson's disease; multiple sclerosis; pain
KM postnatal; anxiety; depression; schizophrenia; dementia; memory loss;
KM mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KM hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KM ulcer; gene; ds

XX	Homo sapiens
OS	

XX	WO200261087-A2
PN	
ur	

PD 08-AUG-2002.

PF 19-DEC-2001; 2001WO-US050107.

PR 19-DEC-2000; 2000US-0257144P.

PA (LIFE-) LIFESPAN BIOSCIENCES INC.

PI Burner GC, Roush CL, Brown JP;

DR WPI; 2003-046718/04.

XX
XX

(GPCR), useful for diagnosing and designing drugs for treating conditions

PT autoimmune diseases.

PS Disclosure; Fig 1; 523pp; English.

The present invention describes antigenic peptides (1) comprising: (a) any one of 1601 sequences (see ABB82019 to ABB93619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (1) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related diseases, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. AB24523 to AB242869 encode GPCR proteins given in ABB1675 to ABB82018, which are used in the exemplification of the present invention

SQ Sequence 3274 BP; 587 A; 979 C; 967 G; 741 T; 0 U; 0 Other;

Query Match	81.6%	Score 41.6	DB 7	Length 3274

Matches	44;	Conservative	0;	Mismatches	4;	Indels	0;	Gaps	0;
---------	-----	--------------	----	------------	----	--------	----	------	----

Oy 4 GATGAGCTGAAGAGGAGGAGGAGGAGAAGTGTGAACCCCAAG 51
|||
Db 892 GAAGAGGAGGAAGAGGAGGAGGAGGAGGAAGTGTGAACCCCAAG 939

RESULT 14
AAD06932
ID AAD06932 standard; cDNA; 593 BP

AC AAD06932;

DT 06-AUG-2001 (first entry)

DE 3' end of human melanoma tumour-associated antigen cDNA from clone 5.31

KW Human; melanoma tumour-associated antigen; cytostatic; gene therapy;

XX

OS	Homo sapiens.
FN	WO200129064-A2.
PD	26-APR-2001.
XX	18-OCT-2000; 2000WO-US041260.
XX	18-OCT-1999; 99US-0160042P.
PR	(UABR-) UAB RES FOUND.
PA	Strong TV, Conry RM, Lobuglio AF;
PI	WPI; 2001-308473/32.
DR	Isolated DNA sequence encoding a melanoma tumor associated antigen,
XX	useful for detection, diagnosis and staging of melanomas, monitoring
PT	metastatic melanomas and as a target for immunotherapy.
XX	Claim 1; Fig 2G; 55pp; English.
PS	The present sequence is 3' end CDNA of clone 5.31 encoding human melanoma
XX	tumour-associated antigen. The CDNA is useful in gene therapy and as an
CC	oligonucleotide probe for detecting mRNA coding for the melanoma tumour-
CC	associated antigen in a sample. The CDNA is useful for vaccinating an
CC	individual who is at risk of getting cancer, suspected of having cancer
CC	or has cancer. The present sequence is useful for inhibiting growth of
CC	melanoma tumour by inducing an immune response against it. The melanoma
CC	tumour-associated antigen is useful for detection, diagnosis and staging
CC	of melanoma, monitoring metastatic melanoma, as new targets for
CC	immunotherapy. The identification of novel tumour antigens may allow
CC	recurrence and metastatic disease to be detected and disease burden
CC	monitored. Characterisation of the melanoma tumour-associated antigen is
XX	of particular use in melanoma research
SQ	Sequence 593 BP; 158 A; 115 C; 146 G; 174 T; 0 U; 0 Other;
Query Match	71.8%; Score 36.6; DB 4; Length 593;
Best Local Similarity	82.4%; Pred. No. 0.56;
Matches	42; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
OY	1 GAGGTGAACCTGAAAGAGAGAGAGAGAGAAGAGTGTGAACCCAG 51
DB	295 GAGGAGAGAGAAAGTAGAGAGAGCGAGAGAGAAAGAGAGTGAACCTCAG 345
RESULT 15	
ABT20256	
ID	ABT20256 standard; DNA; 2367 BP.
XX	
AC	ABT20256;
XX	
DT	16-APR-2003 (first entry)
DE	Aspergillus fumigatus essential gene #2614.
XX	
KW	Fungicide; cytosstatic; essential gene; Aspergillus fumigatus; infection;
KW	cancer; contamination; biofilm; antibody; immune response; ds.
XX	
OS	Aspergillus fumigatus.
PX	WO200286090-A2.
PN	
XX	
PD	31-OCT-2002.
PF	
XX	
PD	23-APR-2002; 2002WO-US013142.
XX	
PR	23-APR-2001; 2001US-0285697P.
XX	
PR	05-JUN-2001; 2001US-0295890P.
XX	
PR	09-JUL-2001; 2001US-0303899P.
XX	
RR	31-AUG-2001; 2001US-0316362P.

XX	(ELIIT-) ELITRA PHARM INC.
PA	Jiang B, Tishkoff D, Zamudio C, Eroshkin AM, Hu W, Lemieux SM,
PI	WPI; 2003-093124/08.
PR	New purified or isolated nucleic acids of essential genes of Aspergillus
PT	fumigatus, useful for treating or preventing infections by A. fumigatus,
PS	or for treating a non-infectious disease in a subject e.g. cancer.
XX	Disclosure; Page; 175pp; English.
XX	The invention relates to novel purified or isolated nucleic acids of
CC	essential genes of Aspergillus fumigatus. The isolated nucleic acids of
CC	the invention are used to treat or prevent infections by a pathogenic
CC	organism such as A. fumigatus, to treat a non-infectious disease in a
CC	subject (e.g. cancer), to prevent or contain contamination of an object
CC	by A. fumigatus, or to prevent or inhibit formation on a surface of a
CC	biofilm comprising A. fumigatus. The polynucleotides are useful for
CC	expressing recombinant protein for characterization, screening or
CC	therapeutic use, as markers for host tissues in which the pathogenic
CC	organisms invade or reside, for comparing with the DNA sequence of A.
CC	fumigatus to identify duplicated genes or paralogues having the same or
CC	similar biochemical activity and/or function, for comparing with DNA
CC	sequences of other related or distant pathogenic organisms to identify
CC	potential orthologous essential or virulence genes, for selecting and
CC	making oligomers for attachment to a nucleic acid array for examination
CC	of expression patterns, for raising anti-protein antibodies, as an
CC	antigen to raise anti-DNA antibodies or to elicit another immune
CC	response, and for identifying polynucleotides encoding the other protein
CC	with which binding occurs or to identify inhibitors of the binding
CC	interaction. The polypeptides may be used to raise antibodies or to
CC	elicit immune response, as a reagent in assays designed to quantitatively
CC	determine levels of the protein in biological fluids, as a marker for
CC	host tissues in which pathogenic organism invade or reside, and to
CC	isolate correlative receptors or ligands in the case of virulence
CC	factors. This polynucleotide sequence represents one of the essential
CC	genes of Aspergillus fumigatus of the invention
SQ	Sequence 2367 BP; 630 A; 644 C; 681 G; 412 T; 0 U; 0 Other;
Query Match	70.6%; Score 36; DB 7; Length 2367;
Best Local Similarity	88.6%; Pred. No. 0.87;
Matches 39; Conservative	0; Mismatches 5; Indels 0; Gaps 0;
OY	1 GAGGATGTAAGTGTAGAGAGACAGAGAGAAGAAAGCTTGA 44
DB	 GAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAAAGTTTGA 2357

```
Search completed: March 2, 2004, 05:39:01
Job time : 268.5 secs
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PF	23-APR-2002; 2002WO-US013142
XX	
PR	23-APR-2001; 2001US-0285697P
PR	27-APR-2001; 2001US-0287066P
PR	05-JUN-2001; 2001US-0295890P
PR	09-JUL-2001; 2001US-0303899P
PR	31-AUG-2001; 2001US-0316362P

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OM nucleic - nucleic search, using ew model

Run on: March 2, 2004, 05:39:14 ; Search time 60 Seconds
(without alignments)
471.708 Million cell updates/sec

Title: US-09-692-077D-2_COPY_880_930

Perfect score: 1 gagagctgaagctgaagagga.....aggaaagctgtgaaccacag 51

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgnt2_6/producta/2/ina/5A_COMB.seq:*
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- 4: /cgnt2_6/producta/2/ina/6B_COMB.seq:*
- 5: /cgnt2_6/producta/2/ina/PCTUS_COMB.seq:*
- 6: /cgnt2_6/producta/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	41.6	81.6	2072 4 US-09-016-434-1181	Sequence 1181, Ap
2	36.6	71.8	593 4 US-09-691-539A-12	Sequence 12, Appl
3	35	1820 5	PCT-US94-09752-1	Sequence 1, Appl
4	34.2	67.1	5125 1 US-08-094-948A-4	Sequence 4, Appl
5	34.2	5125 5	PCT-US96-09319-4	Sequence 4, Appl
6	33	64.7	650 3 US-09-328-111-333	Sequence 333, App
7	32.8	64.3	404 4 US-09-621-976-18769	Sequence 18769, A
8	32.6	63.9	661 4 US-09-894-998A-34	Sequence 34, Appl
9	32.2	63.1	2817 4 US-09-620-312D-1085	Sequence 1085, Ap
10	32.2	63.1	14561 4 US-09-392-714-1	Sequence 1, Appl
11	31.8	62.4	636 4 US-09-702-705-1668	Sequence 1668, Ap
12	31.8	62.4	636 4 US-09-736-457-1668	Sequence 1668, Ap
13	31.8	62.4	636 4 US-09-614-124B-1668	Sequence 1668, Ap
14	31.8	62.4	636 4 US-09-671-325-1668	Sequence 1668, Ap
15	31.6	62.0	258 4 US-09-345-882-21	Sequence 21, Appl
16	31.6	62.0	3211 2 US-08-574-959A-8	Sequence 8, Appl
17	31.6	62.0	3211 2 US-09-357-014-8	Sequence 8, Appl
18	31.6	62.0	3901 2 US-08-574-959A-6	Sequence 6, Appl
19	31.6	62.0	3901 3 US-09-357-014-6	Sequence 6, Appl
20	31.6	62.0	4226 4 US-09-620-313D-480	Sequence 480, App
21	31.6	62.0	6002 4 US-09-345-882-4	Sequence 4, Appl
22	31.6	62.0	162450 4 US-09-345-882-1	Sequence 1, Appl
23	31.4	61.6	2556 4 US-09-817-310-1	Sequence 309, App
24	31.2	61.2	129 4 US-09-702-705-309	Sequence 309, App
25	31.2	61.2	129 4 US-09-736-457-309	Sequence 309, App
26	31.2	61.2	129 4 US-09-614-124B-309	Sequence 309, App
27	31.2	61.2	129 4 US-09-671-325-309	Sequence 309, App

C	28	31.2	61.2	129	4	US-09-589-184-309	Sequence 309, App
	29	31.2	61.2	403	4	US-09-621-976-18731	Sequence 18731, A
	30	31.2	61.2	427	4	US-09-621-976-18711	Sequence 18711, A
	31	31.2	61.2	438	4	US-09-702-705-1028	Sequence 1028, Ap
	32	31.2	61.2	438	4	US-09-736-457-1028	Sequence 1028, Ap
	33	31.2	61.2	438	4	US-09-614-124B-1028	Sequence 1028, Ap
	34	31.2	61.2	438	4	US-09-671-325-1028	Sequence 1028, Ap
	35	31.2	61.2	450	4	US-09-621-976-3667	Sequence 3667, Ap
	36	31.2	61.2	450	4	US-09-621-976-3669	Sequence 3669, Ap
	37	31.2	61.2	459	4	US-09-621-976-1227	Sequence 1227, Ap
	38	31.2	61.2	459	4	US-09-621-976-1224	Sequence 1224, Ap
	39	31.2	61.2	464	4	US-09-621-976-1223	Sequence 1223, Ap
	40	31.2	61.2	464	4	US-09-621-976-3665	Sequence 3665, Ap
	41	31.2	61.2	464	4	US-09-621-976-18757	Sequence 18757, A
	42	31.2	61.2	476	4	US-09-621-976-18704	Sequence 18704, A
	43	31.2	61.2	514	4	US-09-621-976-3661	Sequence 3661, Ap
	44	31.2	61.2	521	4	US-09-621-976-18772	Sequence 18772, A
	45	31.2	61.2	686	4	US-09-166-350-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-09-016-434-1181
Sequence 1181, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREMITH
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1181:
SEQUENCE CHARACTERISTICS:
LENGTH: 2072 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 9178197
US-09-016-434-1181
Query Match 81.6%; Score 41.6; DB 4; Length 2072;
Best Local Similarity 91.7%; Pred. No. 0.0014;

RESULT 2
US-09-69

APPLICANT: Lobuglio, Albert F.
TITLE OF INVENTION: Melanoma Antigens and Methods of Use
FILE REFERENCE: D6253
CURRENT APPLICATION NUMBER: US/09/691,538A
CURRENT FILING DATE: 2000-10-18
PRIOR APPLICATION NUMBER: US 60/160,042
PRIOR FILING DATE: 1999-10-18
NUMBER OF SEQ. ID NOS: 12
SEQ. ID NO. 13

Query Match	71.8%	Score 36.6;	DB 4;	Length 593;
Best Local Similarity	82.4%;	Pred. No. 0.03;		
Matches	42;	Conservative	0;	Mismatches

RESULT 3
CT-US94.

CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey Licata, Esq.
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
STATE: NJ 08003

STATE: NJ
COUNTRY: USA
ZIP: 08002
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
MEDIUM TYPE: STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/09752
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/176,218
FILING DATE: December 30, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/114,951
FILING DATE: August 31, 1993

ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata

Query Match	68.6%	Score 35;	DB 5;	Length 1820;
Best Local Similarity	88.4%	Pred. No. 0.1;		
Matches	38;	Conservative	0;	Mismatches 5.

RESULT 4
US-08-094-9482-4

Sequence 4, Application US/08094948A
Patent No. 5621075
GENERAL INFORMATION:
APPLICANT: Kahn, C. Ronald
APPLICANT: White, Morris F.
APPLICANT: Rothenberg, Paul Louis
TITLE OF INVENTION: INSULIN RECEPTOR SUBSTRATE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lahive & Cockfield
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.

ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC Compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/094,948A
FILING DATE: 21-JULY-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/643,982
FILING DATE: 18-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis (PLM)
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: JDP-013DV
TELECOMMUNICATION INFORMATION:
TEL. NUMBER:

TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 5125 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FRATURE:

NAME/KEY: CDS
LOCATION: 589..4053
-08-094-948A-4

Query Match	67.1%	Score 34.2;	DB 1;	Length 5125;
Best Local Similarity	83.0%;	Pred. No. 0.19;		
Matches 39;	Conservative 0;	Mismatches 8;	Indels 0;	Gaps 0.

;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
;; TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
;; FILE REFERENCE: 210121.538
;; CURRENT APPLICATION NUMBER: US/09/894,998A
;; NUMBER OF SEQ ID NOS: 64
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 34
;; LENGTH: 661
;; TYPE: DNA
;; ORGANISM: HSV-2
US-09-894-998A-34

Query Match 63.9%; Score 32.6; DB 4; Length 661;
Best Local Similarity 89.7%; Pred. No. 0.44;
Matches 35; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAG 39
Db 42 GAGGAGGAGCGCGAAGAGAGAGAGAGAGAGAGAGAG 4

RESULT 9
US-09-620-312D-1085

;; Sequence 1085, Application US/09620312D
;; Patent No. 6569662

;; GENERAL INFORMATION:

;; APPLICANT: Tang, Y. Tom

;; APPLICANT: Liu, Chenghua

;; APPLICANT: Asundi, Vinod

;; APPLICANT: Zhang, Jie

;; APPLICANT: Ren, Feiyan

;; APPLICANT: Chen, Rui-hong

;; APPLICANT: Zhao, Qing A.

;; APPLICANT: Wehrman, Tom

;; APPLICANT: Xue, Aidong J.

;; APPLICANT: Yang, Yonghong

;; APPLICANT: Wang, Jishen-Rui

;; APPLICANT: Zhou, Ping

;; APPLICANT: Ma, Yungqing

;; APPLICANT: Wang, Dunrui

;; APPLICANT: Wang, Zhiwei

;; APPLICANT: John Tillinghaast

;; APPLICANT: Drmanac, Radoje T.

;; TITLE OF INVENTION: No. 6569662el Nucleic Acids and

;; TITLE OF INVENTION: Polypeptides

;; FILE REFERENCE: 784CIP28

;; CURRENT APPLICATION NUMBER: US/09/620,312D

;; CURRENT FILING DATE: 2000-07-19

;; PRIOR APPLICATION NUMBER: 09/552,317

;; FILE REFERENCE: 2000-04-25

;; PRIOR APPLICATION NUMBER: 09/488,725

;; PRIOR FILING DATE: 2000-01-21

;; NUMBER OF SEQ ID NOS: 1105

;; SOFTWARE: PC_FL_genes Version 1.0

;; SEQ ID NO 1085

;; LENGTH: 2817

;; TYPE: DNA

;; ORGANISM: Homo sapiens

;; FEATURE:

;; NAME/KEY: CDS

;; LOCATION: (109)..(2817)

US-09-620-312D-1085

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Best Local Similarity 82.2%; Pred. No. 0.65;
Matches 37; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 2 AGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGTGTGAGC 46
Db 209 AGGGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGACC 253

RESULT 10
US-09-392-714-1

;; Sequence 1, Application US/09392714A

;; Patent No. 6686147

;; GENERAL INFORMATION:

;; APPLICANT: Scanlan, Matthew J.

;; APPLICANT: Gure, All O.

;; APPLICANT: Williamson, Barbara

;; APPLICANT: Chen, Yao-Tseng

;; APPLICANT: Old, Lloyd J.

;; TITLE OF INVENTION: Cancer Associated Antigens and Uses

;; TITLE OF INVENTION: Therfor

;; FILE REFERENCE: L0461/7062

;; CURRENT APPLICATION NUMBER: US/09/392,714A

;; CURRENT FILING DATE: 1999-09-09

;; EARLIER APPLICATION NUMBER: PCT/US98/14679

;; EARLIER FILING DATE: 1998-07-15

;; NUMBER OF SEQ ID NOS: 30

;; SOFTWARE: FastSeq for Windows Version 3.0

;; SEQ ID NO 1

;; LENGTH: 14561

;; TYPE: DNA

;; ORGANISM: Homo sapiens

US-09-392-714-1

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Matches 37; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGTGTGAA 45
Db 6252 GAGGAGGAGAGATGAAGAGAGAGAGAGAGAGAGAGAGATGAA 6296

RESULT 11
US-09-702-705-1668

;; Sequence 1668, Application US/09702705

;; Patent No. 6504010

;; GENERAL INFORMATION:

;; APPLICANT: Wang, Tongtong

;; APPLICANT: Bangur, Chaitanya S.

;; APPLICANT: Lodes, Michael A.

;; APPLICANT: Fanger, Gary

;; APPLICANT: Vedvick, Tom

;; APPLICANT: Carter, Darrick

;; APPLICANT: Retter, Marc

;; APPLICANT: Mannion, Jane

;; APPLICANT: Fan, Liqun

;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

;; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER

;; FILE REFERENCE: 210121.478C14

;; CURRENT APPLICATION NUMBER: US/09/702,705

;; CURRENT FILING DATE: 2000-10-30

;; NUMBER OF SEQ ID NOS: 1833

;; SOFTWARE: FastSeq for Windows Version 3.0

;; SEQ ID NO 1668

;; LENGTH: 636

;; TYPE: DNA

;; ORGANISM: Homo sapiens

US-09-702-705-1668

Query Match 62.4%; Score 31.8; DB 4; Length 636;
Best Local Similarity 76.5%; Pred. No. 0.74;
Matches 39; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGTGTGAACTGCCAG 51
Db 586 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGATATGACTCGAG 636

RESULT 12
US-09-736-457-1668

;; Sequence 1668, Application US/09736457

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1 Patent No.6509448
2 / GENERAL INFORMATION:
3 / APPLICANT: Wang, Tongtong
4 / APPLICANT: Bangur, Chaitanya S.
5 / APPLICANT: Lodes, Michael A.
6 / APPLICANT: Fanger, Gary
7 / APPLICANT: Vedvick, Tom
8 / APPLICANT: Carter, Darrick
9 / APPLICANT: Rector, Marc
10 / APPLICANT: Mannion, Jane
11 / APPLICANT: Fan, Liqun
12 / APPLICANT: Wang, Aijun
13 / TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
14 / TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
15 / FILE REFERENCE: 210121.478C15
16 / CURRENT APPLICATION NUMBER: US/09/736,457
17 / CURRENT FILING DATE: 2000-12-13
18 / NUMBER OF SEQ ID NOS: 1864
19 / SOFTWARE: FaalSeq for Windows Version 3.0
20 / SEQ ID NO 1668
21 / LENGTH: 636
22 / TYPE: DNA
23 / ORGANISM: Homo sapiens
24 / US-09-736-457-1668

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	Best Local Similarity	76.5%	Pred. No. 0.74		
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Db	586	GAGCAGGAAGAAGAGAGAGAGAGAGAGAGAGATGATTATATGACTCGAG	636		

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RESULT 13
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/ Sequence 1668, Application US/09614124B
/ Patent No. 6630574
/ GENERAL INFORMATION:
/ APPLICANT: Mang, Tongtong
/ APPLICANT: Bangur, Chaltanya S.
/ APPLICANT: Lodde, Michael A.
/ APPLICANT: Fanger, Gary
/ APPLICANT: Vedvick, Tom
/ APPLICANT: Carter, Darlick
/ APPLICANT: Retter, Marc
/ APPLICANT: Manion, Jane
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
/ FILE REFERENCE: 210121.478C9
/ CURRENT APPLICATION NUMBER: US/09/614,124B
/ CURRENT FILING DATE: 2001-07-11
/ NUMBER OF SEQ. ID NOS: 1668
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1668
/ LENGTH: 636
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-614-124B-1668

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Best Local Similarity 76.5%;
Matches 39; Conservative 0; Mismatches 12; Indels 0; Gaps 0.

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Dd 586 GAGGAGGAAGAAGAGGAGGAGGAGGATTAATGACTTCGAG 636

RESULT 14
US-09-671-325-1668
; Sequence 1668, Application US/09671325
; Patent No. 6667154

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? GENERAL INFORMATION:
? APPLICANT: Wang, Tonglong
? APPLICANT: Bangur, Chaitanya S.
? APPLICANT: Lodes, Michael A.
? APPLICANT: Fanger, Gary
? APPLICANT: Vedvick, Tom
? APPLICANT: Carter, Darick
? APPLICANT: Retter, Marc
? APPLICANT: Mannoni, Jane
? APPLICANT: Fan, Liqun
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
? TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
? FILE REFERENCE: 210121.478C12
? CURRENT APPLICATION NUMBER: US/09/671,325
? CURRENT FILING DATE: 2000-09-26
? NUMBER OF SEQ ID NOS: 1825
? SOFTWARE: FastSeq for Windows Version 3.0
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? LENGTH: 636
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US-09-671-325-1668

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Query Match	Score	DB	Length
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Indels			0
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RESULT 15
US-09-345-882-21
: Sequence 21, Application US/09345882
: Patent No. 6399373
: GENERAL INFORMATION:
: APPLICANT: Bouquelerelet, Lydie
: TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
: TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
: FILE REFERENCE: GENSER.031A
: CURRENT APPLICATION NUMBER: US/09/345,882
: CURRENT FILING DATE: 1999-06-30
: PRIOR APPLICATION NUMBER: US 60/091,315
: PRIOR FILING DATE: 1998-06-30
: PRIOR APPLICATION NUMBER: US 60/111,909
: PRIOR FILING DATE: 1998-12-10
: NUMBER OF SEQ ID NOS: 140
: SOFTWARE: Patent.pm
: SEQ ID NO 21
: LENGTH: 258
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-345-882-21

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Best Local Similarity 89.5%; Pred. No. 0.77;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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RESULT 14
US-09-671-325-1668
; Sequence 1668, Application US/09671325
; Patent No. 6667154

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US-10-128-714-204  
; Sequence 204, Application US/10128714  
; Publication No. US20030119013A1  
GENERAL INFORMATION:  
APPLICANT: Jiang, Bo  
APPLICANT: Hu, Wengqi  
APPLICANT: Tishkoff, Daniel  
APPLICANT: Zamudio, Carlos  
APPLICANT: Eroshkin, Alexey M  
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and  
FILE REFERENCE: 10182-018-999  
CURRENT APPLICATION NUMBER: US/10/128,714  
PRIORITY FILING DATE: 2002-04-23  
PRIOR APPLICATION NUMBER: US 60/285,697  
PRIOR FILING DATE: 2001-04-23  
PRIOR APPLICATION NUMBER: US 60/287,066  
PRIOR FILING DATE: 2001-04-27  
PRIOR APPLICATION NUMBER: US 60/295,890  
PRIOR FILING DATE: 2001-06-05  
NUMBER OF SEQ ID NOS: 8603  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 204  
LENGTH: 4238  
TYPE: DNA  
ORGANISM: Aspergillus fumigatus  
US-10-128-714-204
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Best Local Similarity 88.6%; Pred. No. 0.038;  
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; Sequence 5204, Application US/10128714  
; Publication No. US20030119013A1  
GENERAL INFORMATION:  
APPLICANT: Jiang, Bo  
APPLICANT: Hu, Wengqi  
APPLICANT: Tishkoff, Daniel  
APPLICANT: Zamudio, Carlos  
APPLICANT: Eroshkin, Alexey M  
APPLICANT: Lemieux, Sebastien M  
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and  
FILE REFERENCE: 10182-018-999  
CURRENT APPLICATION NUMBER: US/10/128,714  
PRIORITY FILING DATE: 2002-04-23  
PRIOR APPLICATION NUMBER: US 60/285,697  
PRIOR FILING DATE: 2001-04-23  
PRIOR APPLICATION NUMBER: US 60/287,066  
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PRIOR APPLICATION NUMBER: US 60/295,890  
PRIOR FILING DATE: 2001-06-05  
NUMBER OF SEQ ID NOS: 8603  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 204  
LENGTH: 4238  
TYPE: DNA  
ORGANISM: Aspergillus fumigatus  
US-10-128-714-5204
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Copyright (c) 1993 - 2004 CompuGen Ltd.

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16	41.6	81.6	481	73	US-60-170-346-61	Sequence 61, App
17	41.6	81.6	516	31	US-09-728-174-4537	Sequence 3537, App
18	41.6	81.6	569	72	US-60-160-189-1492	Sequence 1492, App
19	41.6	81.6	569	72	US-60-160-180-231	Sequence 231, App
20	41.6	81.6	569	72	US-60-160-202-659	Sequence 659, App
21	41.6	81.6	569	72	US-60-160-840-3708	Sequence 3708, App
22	41.6	81.6	569	72	US-60-169-841-1172	Sequence 1172, App
23	41.6	81.6	569	72	US-60-169-842-1193	Sequence 1193, App
24	41.6	81.6	569	72	US-60-169-842-1193	Sequence 3351, App
25	41.6	81.6	601	39	US-60-169-867-3351	Sequence 4865, App
26	41.6	81.6	1353	20	US-09-949-004-865	Sequence 3, App1
27	41.6	81.6	1353	29	US-09-422-98E-3	Sequence 3, App1
28	41.6	81.6	1353	29	US-09-692-077D-1	Sequence 1, App1
29	41.6	81.6	1353	33	US-09-692-077B-1	Sequence 1, App1
30	41.6	81.6	1353	33	US-09-825-923-3	Sequence 3, App1
31	41.6	81.6	1353	43	US-10-001-073-1	Sequence 1, App1
32	41.6	81.6	1353	44	US-10-001-073A-1	Sequence 1, App1
33	41.6	81.6	1353	44	US-10-077-870-3	Sequence 3, App1
34	41.6	81.6	1353	102	US-10-170-235-40719	Sequence 40719, App
35	41.6	81.6	1353	102	US-60-453-050-6437	Sequence 6437, App
36	41.6	81.6	1353	103	US-60-453-135-6437	Sequence 6437, App
37	41.6	81.6	1825	39	US-09-466-412-6437	Sequence 6437, App
38	41.6	81.6	1825	39	US-09-949-004-175	Sequence 6437, App
39	41.6	81.6	2072	49	US-10-305-720-1181	Sequence 175, App
40	41.6	81.6	3655	107	US-10-305-720-1181	Sequence 1181, App
41	41.6	81.6	3655	107	US-60-500-315-891	Sequence 41, App1
42	41.6	81.6	3891	107	US-60-500-315-891	Sequence 890, App
43	41.6	81.6	4050	76	US-60-207-360-68	Sequence 68, App1
44	41.6	81.6	4050	76	US-60-207-360-110	Sequence 110, App
45	41.6	81.6	4050	76	US-60-207-360-110	Sequence 111, App
					US-60-207-360-112	Sequence 112, App

ALIGNMENTS

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1 RESULT US03-03194-4067
2 PCT-US03-03194-4067
3 / Sequence 4067, Application PC/TUS0303194
4 / GENERAL INFORMATION:
5 / APPLICANT: Mendrick, Donna
6 / APPLICANT: Porter, Mark
7 / APPLICANT: Johnson, Kory
8 / APPLICANT: Castle, Arthur
9 / APPLICANT: Blashoff, Michael
10 / APPLICANT: Gene Logic, Inc.
11 / TITLE OF INVENTION: Molecular Hepatotoxicology Modeling
12 / FILE REFERENCE: 44921-5038-01-WO
13 / CURRENT APPLICATION NUMBER: PCT/US03/03194
14 / CURRENT FILING DATE: 2003-01-31
15 / PRIOR APPLICATION NUMBER: US 60/222,040
16 / PRIOR FILING DATE: 2000-07-31
17 / PRIOR APPLICATION NUMBER: US 60/222,880
18 / PRIOR FILING DATE: 2000-11-02
19 / PRIOR APPLICATION NUMBER: US 60/290,029

```

```

; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/331,273
; Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 4295
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4067

LENGTH: 828
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: Genbank Accession No. S67316
PCT-US03-03194-4067

Query Match          100.0%; Score 51; DB 1; Length 828;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches   51; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

Oy      1 GAGGATGAAGCTGAAGAAGAGGAGAGAGAGAGAGAAAGTGTGAACCCCG 51
         |||||||
Db       595 GAGATGAAGCTGAAGAAGAGGAGAGAGAGAGAGAAAGTGTGAACCCCG 645

RESULT 2
US-60-436-643-4067
; Sequence 4067, Application US/60436643
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Caselle, Arthur
APPLICANT: Blaschoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OR INVENTION: Molecular Hepatotoxicology Modeling
FILE REFERENCE: 44921-5038-P15
CURRENT APPLICATION NUMBER: US/60/436,643
CURRENT FILING DATE: 2002-12-30
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/331,273
; Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 4295
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4067
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: LENGTH: 828
: TYPE: DNA
: ORGANISM: Rattus norvegicus
: FEATURE:
: OTHER INFORMATION: Genbank Accession No. S67316
US-60-436-643-4067

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Query Match      100.0%; Score 51; DB 100; Length 828;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Dy 1 GAGGATGAAGCTGAAAGAGAGAGAAGAGAGAAAGTGTGAACCCAC 51
 |||||
Dd 595 GAGGATGAAGCTGAAAGAGAGAGAGAAGAGAGAAAGTGTGAACCCAC 645

RESULT 3
US-60-468-720-1259
; Sequence 1259, Application US/60468720
; GENERAL INFORMATION:

```

APPLICANT: Higgs, Brianon
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Johnson, Kory
APPLICANT: Porter, Mark
APPLICANT: Mendrick, Donna
TITLE OF INVENTION: Nucleic Acid Detection Assay Control Genes
FILE REFERENCE: 449321-5124-P1
CURRENT APPLICATION NUMBER: US 60/468,720
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: US 60/396,145
PRIOR FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 1347
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1259
LENGTH: 828
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURES:
OTHER INFORMATION: Genbank Accession No. S67316
US-60-468-720-1259

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Query Match	100.0%;	Score 51;	DB 103;	Length 828;
Best Local Similarity	100.0%;	Pred. No. 0.019;		
Matches 51; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Oy 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGAAGTGTGAACCCCG 51
Db 595 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGAAGTGTGAACCCCG 645

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RESULT 4
US-09-692-077B-2
; Sequence 2, Application US/09692077B
; GENERAL INFORMATION:
; APPLICANT: Liggett, Stephen
; TITLE OF INVENTION: Alpha-2b-adrenergic receptor polymorphisms
; FILE REFERENCE: Sequences 1-22
; CURRENT APPLICATION NUMBER: US/09/692,077B
; CURRENT FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-692-077B-2

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Query Match      100.0%; Score 51; DB 29; Length 1344;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 GAGGATGAAGCTGAGAGGAGGAGGAGGAGGAGAAGTGTGAACCCCAg 51

Db 880 GAGATGAAGCTGAAGAGGAGGAGGAGGAGAAGTGTGAACCCCAAG 930

RESULT 5
US-09-692-077D-2
; Sequence 2, Application US/09692077D
GENERAL INFORMATION.

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1 GENERAL INFORMATION:
2 APPLICANT: Liggett, Stephen
3 APPLICANT: Small, Kersten M.
4 TITLE OF INVENTION: Alpha-2b-Adrenergic Receptor Polymorphisms
5 FILE REFERENCE: 10738-43
6 CURRENT APPLICATION NUMBER: US/09/692,077D
7 CURRENT FILING DATE: 2000-10-19
8 NUMBER OF SEQ ID NOS: 26
9
10 SOFTWARE: PatentIn version 3.2

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-692-077D-2

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Query Match	100.0%;	Score 51;	DB 29;	Length 1344;
Best Local Similarity	100.0%;	Pred. No. 0.019;		
Matches 51;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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QY      1 GAGATGAAGCTGAAAGAGAGAGAGAAGAGTGTGAACCCAC 51
          |||||
DB      880 GAGATGAAGCTGAAAGAGAGAGAGAAGAGTGTGAACCCAC 930
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RESULT 6
US-10-001-073-2
; Sequence 2, Application US/10001073

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; APPLICANT: Liggett, Stephen
; APPLICANT: Small, Kirsten
; TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
; FILE REFERENCE: 13073-PCT
; CURRENT APPLICATION NUMBER: US/10/001,073
; CURRENT FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-001-073-2

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Query Match	100.0%;	Score 51;	DB 43;	Length 1344;
Best Local Similarity	100.0%;	Pred. No. 0.019;		
Matches 51;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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QY      1 GAGATGAAGCTGAAGAGGAGGAGGAGGAAGAGTGTGAACCCAC 51
      |||||
Db      880 GAGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGAACCCAC 930

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RESULT 7
US-10-001-073A-2
; Sequence 2, Application US/10001073A
Copyright 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649, 2650, 2651, 2652, 2653, 2654, 2655, 2656, 2657, 2658, 2659, 2660, 2661, 2662, 2663, 2664, 2665, 2666, 2667, 2668, 2669, 2670, 2671, 2672, 2673, 2674, 2

1 APPLICANT: Small, Kathleen M.
2
3 TITLE OF INVENTION: Alpha-2 Adrenergic Receptor Polymorphisms
4
5 FILE REFERENCE: 10738-42
6
7 CURRENT APPLICATION NUMBER: US/10/001,073A
8
9 CURRENT FILING DATE: 2001-11-01
10
11 NUMBER OF SEQ ID NOS: 69
12
13 SOFTWARE: Patent version 3.2

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; SEQ ID NO 2
; LENGTH: 1344
; TYPE: DNA

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Query Match	100.0%;	Score 51;	DB 43;	Length 1344;
Best Local Similarity	100.0%;	Pred. No. 0.019;		
Matches	51;	Conservative	0;	Mismatches 0;
				Indels 0

[illegible]

RESULT 8
US-09-692-077D-25

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sequence 25: application US/09692077D
GENERAL INFORMATION:
APPLICANT: Liggett, Stephen
APPLICANT: Small, Kristen M.
TITLE OF INVENTION: Alpha-2b-Adrenergic Re
FILE REFERENCE: 10739-43
CURRENT APPLICATION NUMBER: US/09/692,077D
CURRENT FILING DATE: 2000-10-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.2
SEQ ID NO 25
LENGTH: 60
TYPE: DNA
ORGANISM: Homo sapiens
US-09-692-077D-25

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Query Match          96.1%; Score 49; DB 29; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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Dy 1 GAGGATGAAGCTGAAAGAGAAGAGGAGCGAAGGAAAGTGTCAACCCC 49
| | | | |
Db 12 GAGGATGAAGCTGAAGAGCAGAGGAGGAGGAAAGTGTCAACCCC 60

RESULT 9
US-10-00

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US-10-001-073A-55
? Sequence 55, Application US/10001073A
? GENERAL INFORMATION:
? APPLICANT: Small, Kirsten M.
? APPLICANT: Liggett, Stephen
? TITLE OF INVENTION: Alpha-2 Adrenergic Receptor Polymorphisms
? FILE REFERENCE: 10738-42
? CURRENT APPLICATION NUMBER: US/10/001,073A
? CURRENT FILING DATE: 2001-11-01
? NUMBER OF SEQ ID NOS: 69
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 55
? LENGTH: 60
? TYPE: DNA
? ORGANISM: Homo sapiens
US-10-001-073A-55

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Query Match	96.1%;	Score 49;	DB 43;	Length 60;
Best Local Similarity	100.0%;	Pred. No. 0.06;		
Matches	49;	Conservative	0;	Mismatches

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QY      1 GAGGATGAACCTGAAGAAGAGAGAGAGAGAAAGTGTNAACCC 49  
        |||||  
Db     12 GAGGATGAAGCTGAAGAAGAGAGAGAGAAAGTGTNACCCC 60
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RESULT 10
US-09-422

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; Sequence 1, Application US/09422985
; GENERAL INFORMATION:
; APPLICANT: Snapir, Amir
; APPLICANT: Heinonen, Paula
; APPLICANT: Ahopuro, Pia

```

```

/ APPLICANT: Karvonen, Matti
/ APPLICANT: Koulou, Markku
/ APPLICANT: Pesonen, Ullamari
/ APPLICANT: Scheinin, Mika
/ APPLICANT: Salonen, Jukka T
/ APPLICANT: Tuomainen, Tomi-Pekka
/ APPLICANT: Lakka, Timo A
/ APPLICANT: Nyys"nen, Kristiina
/ APPLICANT: Salonen, Riitta.
/ APPLICANT: Kaunonen, Jussi.
/ APPLICANT: Valkonen, Veli-Pekka
/ TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
/ FILE OF INVENTION: protein, and uses thereof
/ TITLE REFERENCE: Alpha-2B-AR variant
/ CURRENT APPLICATION NUMBER: US/09/422,985
/ CURRENT FILING DATE: 1999-10-22
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 1344
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(1341)
/ OTHER INFORMATION: Coding sequence for variant human
/ OTHER INFORMATION: alpha-2B-adrenoceptor protein
US-09-422-985-1

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Query Match	93.7%	Score 47.8	DB 20	Length 1344
Best Local Similarity	96.1%	Pred. No. 0.11		
Matches 49; Conservative	0	Mismatches 2	Indels 0	Gaps 0

[illegible]

RESULT 11
US-09-825-923-1

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/ sequence 1 Application US/09825923
/ GENERAL INFORMATION:
/ APPLICANT: Snapir, Amir
/ APPLICANT: Heinonen, Paula
/ APPLICANT: Alhopuro, Pia
/ APPLICANT: Karvonen, Matti
/ APPLICANT: Koulu, Markku
/ APPLICANT: Pesonen, Ullamari
/ APPLICANT: Scheinin, Mika
/ APPLICANT: Salonen, Jukka T
/ APPLICANT: Tuomainen, Tomi-Pekka
/ APPLICANT: Lakka, Timo A
/ APPLICANT: Myllynen, Kristiina
/ APPLICANT: Salonen, Raita
/ APPLICANT: Kauphanen, Jussi
/ APPLICANT: Valkonen, Veli-Pekka
/ TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
/ FILE REFERENCE: protein, and uses thereof
/ CURRENT APPLICATION NUMBER: US/09/825,923
/ PRIOR FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 09/422,985
/ PRIOR FILING DATE: 2000-05-25
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 1344
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(1341)
/ OTHER INFORMATION: Coding sequence for variant human

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Dy 5 ATGAAGCTGAAGAGGAGAGAGAGAAGATGTGAACCCAG 51
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Db 370265 AGGAAGTGAAGAGGAGAGAGAAAGATGAAGAACCCAG 370219
| | | | |

Query Match	63.1%	Score 32.2;	DB 6;	Length 1330;
Best Local Similarity	82.2%;	Pred. No. 0.16;		
Matches 37;	Conservative 0;	Mismatches 8;	Indels 0;	Gaps 0

D_b

258 GAGGATGAAGATGCCGACGAGGAGGAGGAGCGAAGAAGTGTCAA 45
302

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RESULT 4
PCT-US04-02188-20
: Sequence 20, Application PC/TUS0402188
: GENERAL INFORMATION:
: APPLICANT: Bayer Pharmaceuticals Corporation
: APPLICANT: Eveleigh, Deepa
: APPLICANT: Bigwood, Douglas
: APPLICANT: Taylor, Ian
: TITLE OF INVENTION: EXPRESSION PROFILES FOR COLON CANCER AND METHODS OF USE
: FILE REFERENCE: 5151
: CURRENT APPLICATION NUMBER: PCT/US04/02188
: CURRENT FILING DATE: 2004-01-23
: PRIOR APPLICATION NUMBER: 60/442,582
: PRIOR FILING DATE: 2003-01-24
: NUMBER OF SEQ ID NOS: 191
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 20
: LENGTH: 3994
: TYPE: DNA
: ORGANISM: Homo sapiens
PCT-US04-02188-20

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Query March      63.1%; Score 32.2; DB 1; Length 3994;
Best Local Similarity 82.2%; Pred. No. 0.18;
Matches 37; Conservative 0; Mismatches 8; Indels 0; Gaps 0
```

Dy 1 GAGGATTAACCTGAAGAAGAGAGAGAGAGAGAAAGTGTGGAA 45
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 926 GAGAGGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 970

```

RESULT 5
US-10-764-425-20
/ Sequence 20. Application US/10764425
/ GENERAL INFORMATION:
/ APPLICANT: Bayer Pharmaceuticals Corporation
/ APPLICANT: Eweleigh, Deepa
/ APPLICANT: Bigwood, Douglas
/ APPLICANT: Taylor, Ian
/ TITLE OF INVENTION: EXPRESSION PROFILES FOR COLON CANCER AND METHODS OF USE
/ FILE REFERENCE: 5151
/ CURRENT APPLICATION NUMBER: US/10/764,425
/ CURRENT FILING DATE: 2004-01-23
/ PRIOR APPLICATION NUMBER: 60/442,582
/ PRIOR FILING DATE: 2003-01-24
/ NUMBER OF SEQ ID NOS: 191
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 20
/ LENGTH: 3994
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-764-425-20

```

Query Match	63.1%;	Score 32.2;	DB 6;	Length 3994;
Best Local Similarity	82.2%;	Pred. No. 0.18;		
Matches 37;	Conservative 0;	Mismatches 8;	Indels 0;	Gaps 0

DY 1 GAGGATGAACCTGTAAAGAGAGCGAGCGAGCGAAGACTGTGAA 45
 |||||
Dδ 926 GAGCGAGAAAGAAAGAAAGAGAGAGCGAGCGAAGACGAGAAGA 970
 |||||

```

RESULT 6
PCT-US03-32805-1
; Sequence 1, Application PC/TUS0332805
; GENERAL INFORMATION:
; APPLICANT: decode genetics ehf.
; APPLICANT: Helgadottir, Anna
; APPLICANT: Gulcher, Jeffrey R.
; APPLICANT: Manolescu, Andrei
; TITLE OF INVENTION: Susceptibility Gene for Myocardial
; TITLE OF INVENTION: Infarction
; FILE REFERENCE: 2345..2048002
; CURRENT APPLICATION NUMBER: PCT/US03/32805
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/419,432
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 398800
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (70677)...(70776)
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (154988)..(155087)
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 248521
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (269591)..(270091)
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (272544)..(272643)

```

```

1 OTHER INFORMATION: n = A,T,C or G
2 FEATURE:
3 NAME/KEY: misc_feature
4 LOCATION: (1279545)...(1279644)
5 OTHER INFORMATION: n = A,T,C or G
6 FEATURE:
7 NAME/KEY: misc_feature
8 LOCATION: (300892)...(300991)
9 OTHER INFORMATION: n = A,T,C or G
10 FEATURE:
11 NAME/KEY: misc_feature
12 LOCATION: (327555)...(327654)
13 OTHER INFORMATION: n = A,T,C or G
14 FEATURE:
15 NAME/KEY: misc_feature
16 LOCATION: (333849)...(333948)
17 OTHER INFORMATION: n = A,T,C or G
18 FEATURE:
19 NAME/KEY: misc_feature
20 LOCATION: (341698)...(341698)
21 OTHER INFORMATION: n = A,T,C or G
22 FEATURE:
23 NAME/KEY: misc_feature
24 LOCATION: (345190)...(345289)
25 OTHER INFORMATION: n = A,T,C or G
26 FEATURE:
27 NAME/KEY: misc_feature
28 LOCATION: (350504)...(350603)
29 OTHER INFORMATION: n = A,T,C or G
30 FEATURE:
31 NAME/KEY: misc_feature
32 LOCATION: (391524)...(391623)
33 OTHER INFORMATION: n = A,T,C or G
34 FEATURE:
35 NAME/KEY: misc_feature
36 LOCATION: (396625)...(396724)
37 OTHER INFORMATION: n = A,T,C or G
38 CCT-USB3-32805-1

```

Query March	63.1%	Score 32.2;	DB 1;	Length 398800;
Best Local Similarity	82.2%	Pred. No. 0.28;		
Matches 37; Conservative	0;	Mismatches	8;	Indels 0;
				Gaps 0;

QY 1 GAGGATGAAGCTGAACAGAGAGAGACGAGAGGAAGCTGTGAA 45
 Db 51865 GATGAGGAAGATGAAGAGGATGAGAGCGAGAGGAAGTGAAGAA 51909

```

RESULT 7
US-10-767-701-29063/c
/ Sequence 29063, Application US/10767701
/ GENERAL INFORMATION:
/
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
/ FILE REFERENCE: 38-21(5353)B
/ CURRENT APPLICATION NUMBER: US/10/767,701
/ CURRENT FILING DATE: 2004-01-29
/ NUMBER OF SEQ ID NOS: 63128
/
/ SEQ ID NO 29063
/
/ LENGTH: 353
/
/ TYPE: DNA
/
/ ORGANISM: Sorghum bicolor
/
/ FEATURE:
/
/ OTHER INFORMATION: Clone ID: 8548511
/
/ US-10-767-701-29063

```

Query March Similarity 61.2%; Score 31.2; DB 6; Length 353;
Beet Local Similarity 81.8%; Pred. No. 0.27; 8; Indels 0; Gaps 0;
Matches 36; Conservative 0; Mismatch 0;

Oy 1 GAGGATGAAGCTGAACAAGAAGAGAGAGAGAAAGTGTCA 44
Db 257 GACGGTGAAGCGCAAGAGAGCAGGATGAGAGAGAAAGCCGA 214

RESULT 8
US-10-417-375A-125

; Sequence 125, Application US/10417375A
; GENERAL INFORMATION:

APPLICANT: David W. Morris
APPLICANT: Marc Malandro

FILE REFERENCE: 529452001600

FILE REFERENCE: 529452001800
CURRENT APPLICATION NUMBER: US/10/417,375A
CURRENT FILING DATE: 2003-04-15

```

; CURRENT FILING DATE: 2003-04-15
; NUMBER OF SEQ ID NOS: 176

```

```

; SOFTWARE: FastSeq for Windows Version 4.0
;
; SEO ID NO 125

```

LENGTH: 188053
TYPE: DNA

```

;
; TYPE: DNA
; ORGANISM: Mus musculus
;

```

```
;; FEATURE:
;; NAME/KEY: misc_feature
```

LOCATION: (1) .. (188053)
OTHER INFORMATION: n = A, T, C or G

US-10-417-375A-125

Query Match	61.24	Score	31.2	DB	6	Length	188053
Best Local Similarity	81.84	Pred.	No. 0.5				
Matches	36	Conservative	0	Mismatches	8	Indels	0
						Gaps	0

Qy 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGAAGTGTGA 44
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 63527 GAGCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGGGGA 63570

RESULT 9
US-10-767-471-10681/c

; Sequence 10681, Application US/10767471
; GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al
TITLE OF INVENTION: GENETIC POLYMER

TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF

```

; FILE REFERENCE: CL001505
; CURRENT APPLICATION NUMBER: US/10/767,471

```

; CURRENT FILING DATE: 2004-01-30
 ; NUMBER OF SEO ID NOS: 50231

```

SOFTWARE: FastSeq for Windows Version 4.0
;
; SEQ ID NO 10681

```

```

; SEQ ID NO 10681
; LENGTH: 209320
;

```

```

;      TYPE: DNA
;      ORGANISM: Homo sapiens

```

```

FEATURE:
NAME/KEY: misc feature

```

LOCATION: (1) .. (209320)

OTHER INFORMATION: H A, I, C OF G, OF INSERTION/DELETION POLYMERIZATION (SEE PAPERS 1-3)
US-10-767-471-10681

Query Match	61.2%	Score 31.2;	DB 6;	Length 209320;
Best Local Similarity	81.8%;	Pred. No. 0.5;		
Matches 36;	Conservative 0;	Mismatches 8;	Indels 0;	Gaps 0;

[illegible]

RESULT 10

US-10-767-701-26619/c
: Sequence 26619, Application US/10767701

APPLICANT: Kovalic David K

APPLICANT: Zhou, Yihua

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REFERENCE	2 (bases 1 to 872)
AUTHORS	Hunter,C.
TITLE	Direct Submision
JOURNAL	Submitted (14-Sep-2001) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. UK Email: biolhelp@hmp.mrc.ac.uk
FEATURES	Location/Qualifiers
SOURCE	1..872 /organism="Equus caballus" /mol_type="genomic DNA" /db_xref="taxon:9796"
ORIGIN	
Query Match	74.9% Score 38.2; DB 29; Length 872;
Best Local Similarity	84.3%; Pred. No. 55;
Matches	43; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Dn	592 GAGGATGAAGCTGAAGACGAGAGAGAGAGAAGAGTGTGAACCCAG 51 592 GAGGAAGCGAGGAGGAGGAGGAGGAGGGGAGGAAGTGTCGAGCCTCAG 642
RESULT 5	
LOCUS	AL872808
DEFINITION	AL872808 XGC-egg Silurana tropicalis cDNA clone Tgsg106k18 5', mRNA sequence.
ACCESSION	AL872808
VERSION	AL872808.2 GI:38666205
KEYWORDS	EST.
SOURCE	Silurana tropicalis (western clawed frog)
ORGANISM	Silurana tropicalis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae; Xenopodinae; Silurana. 1 (bases 1 to 633) Croining,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J. Sanger Xenopus tropicalis EST project 2001 (11_2003) Unpublished (2003) On Sep 15, 2002 this sequence version replaced gi:22893073. Contact: Taylor R Sanger Institute Hinxton, Cambridgeshire, CB10 1SA, UK Email: trop@sanger.ac.uk Sanger Xenopus tropicalis EST project 2001 TROPICALIS_SEQUENCE_ID: Tgsg106k18.p1ks6 Sequencing primer: SP6 This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn. cDNA was oligo dt primed from 5ug of poly A+ RNA from egg. ECORI-NciI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NciI at the 3' end. Vector: pCS107; Site_1: EcoRI; Site_2: NciI Host: Escherichia coli XL1-blue. Location/Qualifiers 1..633 /organism="Silurana tropicalis" /mol_type="mRNA" /db_xref="taxon:9364" /clone="Tgsg106k18" /dev stage="egg" /lab host="Escherichia coli XL1-blue" /note="vector: pCS107; Site_1: EcoRI; Site_2: NciI. cDNA was oligo dt primed from 5ug of poly A+ RNA from egg. ECORI-NciI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NciI at the 3' end"
FEATURES	
SOURCE	
ORIGIN	
Query Match	74.1% Score 37.8; DB 9; Length 633;
Best Local Similarity	85.7%; Pred. No. 64;
Matches	42; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy	1	GAGGATTAAGCTGAAGAGAGAAGAGAAGAGAAGTGTGAACCC	49
Dd	559	GTGATGTAAGTGAAGAGAAGAGTAGAGAGATGAAGTGTGAACCA	511
RESULT 6			
LOCUS	AL852740/c	634 bp	mRNA linear EST 26-NOV-2003
DEFINITION	AL852740 XGC-egg Silurana tropicalis cDNA clone TEG9015d14 5', mRNA sequence.		
ACCESSION	AL852740		
VERSION	AL852740.2	GI:38563553	
KEYWORDS	EST.		
SOURCE	Silurana tropicalis (western clawed frog)		
ORGANISM	Silurana tropicalis Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Silurana. 1 (bases 1 to 634)		
REFERENCE	Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J. Sanger Xenopus tropicalis EST project 2001 (11_2003) Unpublished (2003) On Sep 15, 2002 this sequence version replaced gi:22872961. Contact : Taylor R Sanger Institute Hinxton, Cambridgeshire, CB10 1SA, UK Email: trop@sanger.ac.uk Sanger Xenopus tropicalis EST project 2001 TROPICALIS SEQUENCE ID: TEG9015d14.plkSP6 Sequencing primer: SP6 This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn. cDNA was oligo dt primed from sug of poly A+ RNA from egg. ECORI-NciI cut cDNA was then ligated into pCS107 with ECORI at the 5' end and NciI at the 3' end. Vector: pCS107; Site1: ECORI; Site2: NciI Host: Escherichia coli XL1-blue. Location/Qualifiers 1..634		
FEATURES			
source	/organism="Silurana tropicalis" /mol_type="mRNA" /db_xref="taxon:8364" /clone="TEG9015d14" /dev_stage="egg" /lab_host="Escherichia coli XL1-blue" /clone_lid="XGC-egg" /note="vector: pCS107; Site 1: ECORI; Site 2: NciI; cDNA was oligo dt primed from sug of poly A+ RNA from egg. ECORI-NciI cut cDNA was then ligated into pCS107 with ECORI at the 5' end and NciI at the 3' end"		
ORIGIN			
Query Match	74.1%; Score 37.8; DB 9; Length 634;		
Best Local Similarity	85.7%; Pred. No. 64;		
Matches	42; Conservative 0; Mismatches 7; Indels 0; Gaps 0;		
Oy	1	GAGGATTAAGCTGAAGAGAGAAGAGAAGAGAAGTGTGAACCCC	49
Dd	204	GTGATGTAAGTGAAGAGAAGAGTAGAGATGAAGTGTGAACCA	156
RESULT 7			
LOCUS	CF360731/c	642 bp	mRNA linear EST 25-AUG-2003
DEFINITION	CF360731 MARC 3Pig Sus scrofa cDNA 3', mRNA sequence.		
ACCESSION	CF360731		
VERSION	CF360731.1	GI:34158729	
KEYWORDS	EST.		
SOURCE	Sus scrofa (pig)		
ORGANISM	Sus scrofa Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 642)		
REFERENCE			

AUTHORS Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Fox,J.,
 Wise,T.A., Nommeman,D.J., Wray,J.E. and Keeler,J.W.
 TITLE A second set of porcine ESTs from a pooled-tissue normalized
 library
 JOURNAL Unpublished (2003)
 COMMENT Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
 cross match v0.990329.
 Plate: SRG8014 row: 0 Column: 4
 Seq primer: TAGAAGCACACTCGAGG.
 Location/Qualifiers
 1..642
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 3Pig"
 /note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
 library made with RNA pooled from multiple tissues
 including brain, liver, muscle, placenta/endometrium,
 ovary, testes, and bone marrow."
 ORIGIN
 Query Match 72.5% Score 37 DB 14 Length 642;
 Best Local Similarity 88.9% Pred. No. 96;
 Matches 40; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Oy 1 GAGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGTGTGAA 45
 Db 377 GAGGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGA 333
 RESULT 8 787 bp mRNA linear EST 10-OCT-2002
 LOCUS BU748295
 DEFINITION CH3#019 B01T7 Canine heart normalized cDNA library in pBluescript
 LOCUS BU748295
 ACCESSION BU748295
 VERSION BU748295.1 GI:23700479
 KEYWORDS EST.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 1 (bases 1 to 787)
 Y1.Y., Desai,R., Olate,M., Henthorn,P. and George A.L.
 Expressed sequence tags from Canine heart
 Unpublished (2003)
 Other ESTs: CH3#019_B01T3
 Contact: George AL
 Division of Genetic Medicine
 Vanderbilt University
 559 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA
 Tel: 615 936 2660
 Fax: 615 936 2661
 Email: al.george@vanderbilt.edu
 Insert length: 1072 Std Error: 0.00
 Seq primer: T7: TAATACGACTCACTATAGGG
 High quality sequence start: 41
 High quality sequence stop: 785.
 Location/Qualifiers
 1..787
 /organism="Canis familiaris"
 /mol_type="mRNA"
 /db_xref="taxon:9615"
 /clone="CH3#019_B01"

/tissue_type="heart"
 /cell_type="heart"
 /dev_stage="mixed developmental stages (adult, 30 day - 40
 day fetal)"
 /clone_lib="Canine heart normalized cDNA library in
 pBluescript"
 /note="Organ: heart; Vector: pBluescript; Site_1: 5' of
 vector NotI; Site_2: 3' of vector EcoRI; Tissue source:
 dog heart (adult, 30 day - 40 day fetal), right and left
 atria and ventricle. Dog breed - mixed (beagle, German
 shepherd, pointer, Irish setter). Library construction:
 oligo-dT primed"

Query Match	72.5%	Score 37	DB 13	Length 787
Best Local Similarity	88.9%	Pred. No. 99		
Matches	40	Conservative 0	Mismatches 5	Indels 0 Gaps 0

```

Qy      1  GAGCATGAAGCTGAAAGAGAGAGAGAGAGAGAAGAGTGTCGAA 45
          ||| | | | | | | | | | | | | | | | | | | | |
Db      41  GATGAAGAAGCAGAAAGAGAGAGAGAGAGAGAGAGAGATCAA 85
  
```

RESULT 9
 BZ195097/c
 LOCUS
 DEFINITION CH230-248P14.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone
 ACCESSION BZ195097
 VERSION BZ195097.1 GI:23853149
 KEYWORDS GSS.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 REFERENCE Rattus norvegicus
 AUTHORS Karyota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (baaes 1 to 770)
 Zhao,S., Shetty,J., Shatman,S., Tsagaye,G., Geer,K.,
 Shvartbeyn,A., Gregorogis,E., Overton,L., Russell,D., Chen,D.,
 Riggs,F., de Jong,P. and Fraser,C.M.
 Rat BAC End Sequences from Library CHORI-230 Mbci segment
 Unpublished (1999)
 Other_GSSs: CH230-248P14.TJ
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the rat BAC library CHORI-230
 (<http://www.chori.org/bacpac/rat230.htm>). For BAC library
 availability, please contact Pieter de Jong (pdejong@gmail.com).
 Clones may be purchased from BACPAC Resources
 (<http://www.chori.org/bacpac/orcetinginformation.htm>). BAC end
 page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
 Plate: 248 row: P column: 14
 Seq primer: T7
 Class: BAC ends.

FEATURES
 source
 Location/Qualifiers
 1..770
 /organism="Rattus norvegicus"
 /mol_type="genomic DNA"
 /strain="BN/SsNHsd/MCM"
 /db_xref="taxon:10116"
 /clone="CH230-248P14"
 /sex="Female"
 /cell_type="Brain"
 /clone_lib="CHORI-230 Segment 2"
 /note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
 CHORI-230 Rat (BN/SsNHsd/MCM) BAC library produced by
 Pieter de Jong"

Query Match	71.0%	Score 36.2;	DB 14;	Length 256;
Best Local Similarity	83.7%	Pred. No. 1.3e+02;		
Matches 41; Conservative	0;	Mismatches 8;	Indels 0;	Gaps 0;

ACCESSION
CIB625989
VERSION
CIB625989.1
KEYWORDS
EST.
GI:29620978

```
Query Match      69.4%; Score 35.4; DB 12; Length 365;
Best Local Similarity 86.7%; Pred. No. 2e+02;
Matches 39; Conservative 0; Mismatches 6; Indels 0; Gaps 0
```

QY 1 GAGGATGAAGCTGAGAGGAGGAGGAGGAGGAGAGTGTGAA 45
 |||||
 DB 149 GAGGAGGAAGATGAGGAGGAGGAGGAGGAGGAAGAGAGAGTGA 105

RESULT 15

B0294503

LOCUS B0294503 378 bp mRNA linear EST 15-MAY-2002

DEFINITION Pa002 Periplaneta americana Lambda Express library Periplaneta americana cDNA clone 5, mRNA sequence.

ACCESSION B0294503

VERSION B0294503.1 GI:20803437

KEYWORDS EST

SOURCE Periplaneta americana (American cockroach)

ORGANISM

Periplaneta americana
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattellidae;
 Blattidae; Periplaneta.

1 (bases 1 to 378)

Zhou, Z.W., Liu, Z.G. and Gao, B.

The construction of Periplaneta americana nymph cDNA library and
 IgG4 immunology screen
 Unpublished (2002)

JOURNAL

COMMENT

Immunology Department

Jiang Xi Medical College

106, Bayi Street, Nanchang, Jiangxi, P.R.C.

Tel: 86-0791-6363001

Email: Zhouzhenwen28@hotmail.com.

Location/Qualifiers

FEATURES

source

1..378

/organism="Periplaneta americana"

/mol_type="mRNA"

/db_xref="taxon:6978"

/clone="5"

/tissue_type="whole body"

/dev_stage="nymph"

/lab_host="E.coli NM522"

/clone_lib="Periplaneta americana lambda Express library"

/note="Vector: lambda Excell; These sequences were
 screened by cockroach sensitive patients' IgG4 serum "

ORIGIN

Query Match 69.4%; Score 35.4; DB 13; Length 378;

Best Local Similarity 86.7%; Pred. No. 2e+02;

Matches 39; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAGAGGAGGAGGAGGAGGAGGAGAGTGTGAA 45
 |||||

DB 159 GAGGAGGAAGCTGAGAGGAGGAGGAGGAGGAGGAAGAGAGAGAA 203

Search completed: March 2, 2004, 08:34:35
 Job time : 2156 secs

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